

Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995
 DEFINITION Human DNase I mRNA, complete cds.
 ACCESSION M55983
 VERSION M55983.1 GI:181623
 KEYWORDS DNase I.
 SOURCE Human pancreas, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 FEATURES Location/Qualifiers
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 CDS 160..1008
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 mat peptide 226..1005
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 BASE COUNT 226 a 305 c 282 g 226 t
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 121 catttcgtc atctctgagg acatcaccat catctcgagg tgagggcat gaagctgtc
 181 gggcgctgc tggcactggc ggcctactg cagggggccg tgcctgaa gatcgccagcc
 241 ttcaacatcc agacattttgg ggagaccaag atgtccaatg ccaccctcgat cagctacatt
 301 gtgcagatcc tgagccgcta tgacatcgcc ctggccagg aggtcagaga cagccaccc
 361 actgccgtgg ggaagctgtc ggacaaccc aatcaggatg caccagacac ctatca
 421 gtggtcagtgc agccactggg acggaaacagc tataaggagc gctacccgtt cgtgtacagg
 481 cctgaccagg tggctgcgtt ggacagctac tactacatg atggctgcga gcccctgcggg
 541 aacgacaccc tcaaccgaga gccagccatt gtcagggttct tctcccggtt cacagagg
 601 agggagtttgc cattgttcc cttgcgtcg gccccgggggg acgcgtatgc cgagatcgac
 661 gctctctatgc acgtctacttggatgtccaa gagaatggg gcttggagga cgtcatgtt
 721 atgggcact tcaatgcggg ctgcagctat gtgagaccct cccagggc atccatccgc
 781 ctgtggacaa gccccaccc ttccatgtcg atccccgaca ggcgtacac cacagctaca
 841 cccacgcact gtgcctatga caggatcgatg gttcaggaga tgctgtccg aggcgcgtt
 901 gttcccgact cggctcttcc tttaacttc caggctgcct atggcctgag tgaccaactg
 961 gccccaggcca tcagtgcacca ctatccatgt gagggtatgc tgaagtgc agccccctccc
 1021 cacaccaggatg gaactgcag
 //

Fig. 1

Human DNase I construct

LOCUS MHDNASE.DN 783 bp mRNA PRI 06-MAR-1995
DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove Narl site
ACCESSION M55983
NID g181623
KEYWORDS DNase I.
SOURCE Human pancreas, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
FEATURES Location/Qualifiers
source 1. .1039
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hDNase-18-1"
/tissue_type="pancreas"
sig_peptide 160. .225
/gene="DNase I"
CDS 160. .1008
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/db_xref="PID:g181624"
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VDSYYDGCEPCGNDT
FNREPAIVRFFSRFTEVREFAIVPLA
APGD
AVAEI
DALYDVYLDVQE
KWGL
EDV
MLMGDFNAGCSYVRPSQWSSIRLWT
SPTFQWLIP
SDADTTAT
PTHCAYD
RIVVAG
MLLRGAVV
PDSALPFNFQ
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HYP
VEV
MLK"
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BASE COUNT 168 a 236 c 220 g 159 t
ORIGIN

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61 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
121 AGAGACAGCC ACCTGACTGC CGTGGGGAAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
241 CTGTTCTGTG ACAGGGCTGA CCAGGTGTCT GCGGGTGGACA GCTACTACTA CGATGATGGC
301 TGCAGGCCCT GCGGGAACGA CACCTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
361 CGGTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCTGCG ATGCCGCCCG GGGGGACGCA
421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
481 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
541 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
661 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
721 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
781 TGA

//

Fig. 2(A)

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 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 source <10..>75
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 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas [Split]"
 sig_peptide 10..75
 /gene="DNase I"
 CDS 10..>75
 /gene="DNase I"
 /codon_start="1"
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 /db_xref="PID:g181624"

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 gene 10..>75
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 /note="1 to 783 of mod humanDNaseI"
 frag 76..858
 /note="1 to 72 of 104linker"
 frag join(76..>129,<131..147)
 /note="1 to 72 of 103linker [Split]"
 frag join(76..>126,<127..>129,<131..147)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER
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 61 CAGGGGGCCG TGTCCTGAA GATCGCAGCC TTCAACATCC AGACATTGG GGAGACCAAG
 121 ATGTCCAATG CCACCCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
 181 CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
 241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
 301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
 361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
 421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTG CCATTGTTCC CCTGCATGCG
 481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
 541 GAGAAATGGG GCTTGAGGA CGTCATGTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
 601 GTGAGACCCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCCACCTT CCAGTGGCTG
 661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
 721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCGACT CGGCTCTTCC CTTAACTTC
 781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
 841 GAGGTGATGC TGAAGTGA

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Fig. 2(B)

pAS6 – light chain

LOCUS HMFG1LC2.D 721 bp DNA
DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER. 18-AUG-1998
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (BASES 1 TO 342)
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT SCANNED IN FROM JOURNAL
FEATURES
SITES

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to R133 silent mutation (T in Verhoeven paper)

BASE COUNT 197 a 202 c 182 g 140 t
ORIGIN ?

x LEADER SEQ
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGAACAG CTACAGGTGT CCACTCGGAC
61 ATCCAGATGA CCCAGAGGCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC
121 ACCTGTAAGT CCAGTCAGAG CCTTTTATAT AGTAGCAATC AAAAGATCTA CTTGGCCTGG
181 TACCAAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA
241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTA CCGACTTCAC CTTCACCATC
301 AGCAGCCTCC AGCCAGAGGA CATCGCCACC TACTACTGCC AGCAATATTA TAGATATCCT
361 CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA CTGTGGCTGC ACCATCTGTC
421 TTCATCTTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG
481 CTGAATAACT TCTATCCCAG AGAGGCCAAA GTACAGTGGAA AGGTGGATAA CGCCCTCCAA
541 TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAAGTCTA CGCCTGCGAA
661 GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAAGAGCT TCAACAGGGG AGAGTGTAG
721 A

//

Fig. 3(A)

LOCUS HHMFG1KLC_ 730 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..730 /note="1 to 721 of hHMFG1light chain"
 frag 10..730 /note="1 to 72 of 104linker"
 frag join(10..>63,<65..81) /note="1 to 72 of 103linker [Split]"
 frag join(10..>60,<61..>63,<65..81) /note="1 to 78 of 102linker [Split]"
 BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER
 ORIGIN -
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 61 CACTCCGACA TCCAGATGAC CCAGAGCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
 121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
 181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
 241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTG AGCGGTAGCG GTAGCGGTAC CGACTTCACC
 301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
 361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 601 TACAGCCTCA GCAGCACCCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 721 GAGTGTAGA

//

Fig. 3(B)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCIILFLVATATGVHSDIQMTQSPSSLSASVGDRVVTITCKSSQL
LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT
DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI
FPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYLSSTTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC

Fig. 3(C)

pAS6 – heavy chain

LOCUS HHMFG1HC.D 1404 bp DNA
DEFINITION HUMANISED HMFG1 heavy chain
ACCESSION HHMFG1H
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT VH domain SCANNED IN FROM JOURNAL
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
SITES Note
BASE COUNT 333 a 439 c 379 g 253 t
ORIGIN ?

14-AUG-1998

LEADER

1 ATGGGATGGA GCTGTATCAT CCTCTCTTGT GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTG TGAGGACACA GCGGTCTATT ACTGTCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGTGAC CGTGCCTCTCC AGCAGCTTG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCACTC
781 TTCCCTCTTCC CCCCCAAAAAC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGCA CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA ATGA

Antibody DNase Fusions Made Here
(eg pAS34----39.)

→ End of lower hinge region of heavy chain. PAPE Amino Acid Seq. Fab'₂ fusions were made at this point.

Those with HYBRID HINGES are altered further up
i.e.

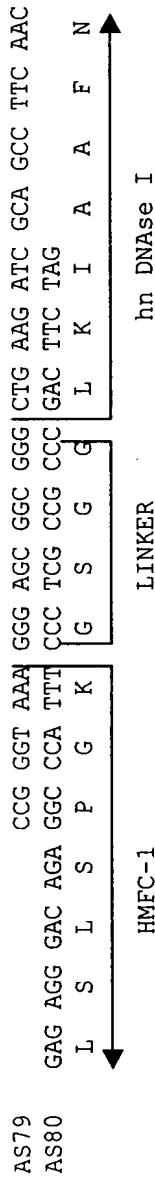
→ This part GACAAAAACTGACACA
D K T H T

After this sequence you get the HYBRID HINGE + LINKER SEQUENCES
Then DNase I (eg Fab-DNase construct pAS302)

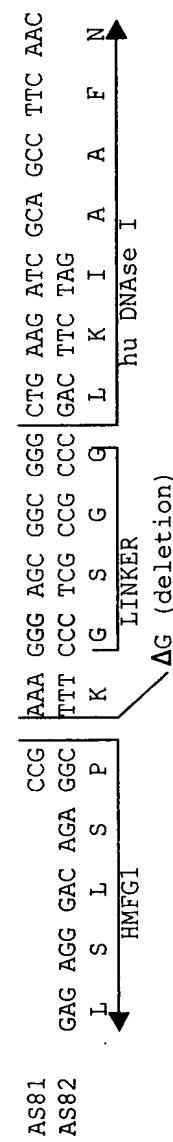
Fig. 3(D)

Oligos involved in the fusion of whole antibody-DNase

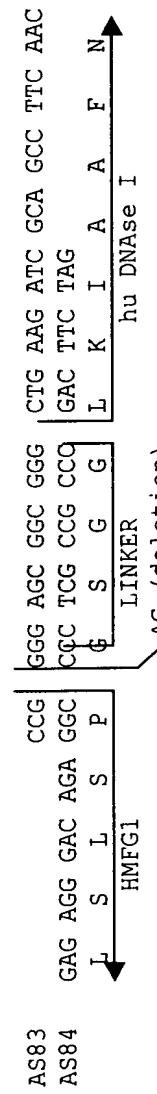
Constructs PAS34/37



Constructs PAS35/38

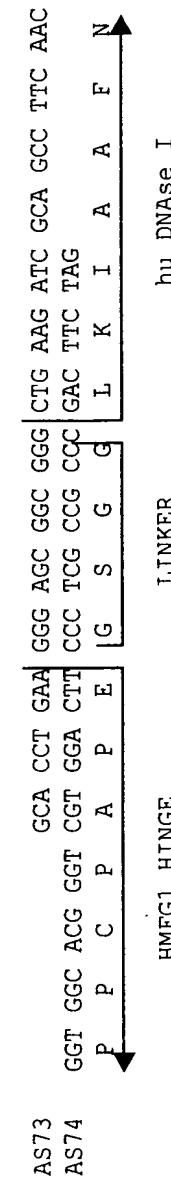


Constructs PAS36/39



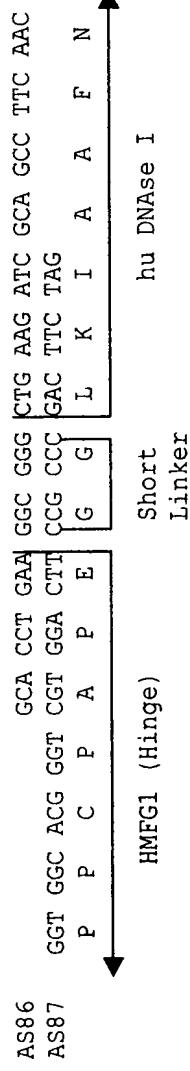
Oligos involved in the fusion of Fab'2-DNaseI

Constructs PAS23/27

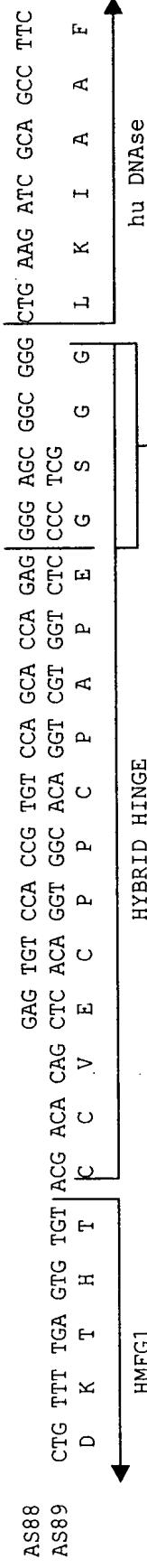


Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

Constructs pAS101/105



Constructs pAS102/106



Constructs pAS103/107

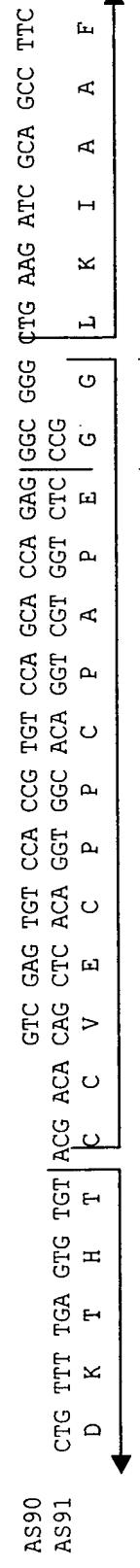


Fig. 4(B)

pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 434 g 308 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGAG TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAG **GGAGCGGCAG** GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTGT
1021 TACAGGCCTG ACCAGGTGTC TGCCTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCAGGAAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTCTTCTC CCGGTTACA
1141 GAGGTCAAGGG AGTTGCCAT TGTTCCCTG CATGCGGCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCCTGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

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Fig. 5(A)

LOCUS FDDNASE23_ 1554 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 /note="1 to 66 of 23/27linker"
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 /note="1 to 78 of 102linker [Split]"
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAAGGG GGAGCGCCGG GCTGAAGATC
 781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
 901 CACCTGACTG CCGTGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTGT
 1021 TACAGGCCTG ACCAGGTGTC TCGGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
 1081 TGCAGGAACG ACACCTCAA CCGAGAGCCA GCCATTGTCA GGTCTCTC CCGGTTACAA
 1141 GAGGTCAGGG AGTTGCCAT TGTTCCCTG CATGCGGCC CGGGGACGC AGTAGCCGAG
 1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
 1261 ATGTTGATGG GCGACTTCAA TGCAGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
 1321 ATCCGCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCAACA
 1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
 1441 GCCGTTGTTG CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
 1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

//

Fig. 5(B)

LOCUS FDDNASE23K 1563 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 /note="1 to 1554 of 23.dna [Split]"
 frag 730..795
 /note="1 to 66 of 23/27linker"
 frag join(730..>744,<745..795)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 472 C 437 G 309 T 0 OTHER
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCTGG GGCCTCAGTG
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTGC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT CTGTGCAAGA
 361 TCCTACGACT TTGCTCTGGTT TGCTTACTGG GGCAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACCGT GTGCCCTCCA GCAGCTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCC
 781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 841 CTCGTCAAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 901 AGAGACAGCC ACCTGACTGC CGTGGGAAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
 961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
 1021 CTGTCGTTG ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
 1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
 1141 CGGTTCACAG AGGTCAAGGG GTTTGCCTATT GTTCCCTGC ATGCGCCCC GGGGGACGCA
 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCCTCCAGT GGCTGATCCC CGACAGCGCT
 1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCTTTA ACTTCAGGC TGCCTATGGC
 1501 CTGAGTGACCA AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 1561 TGA
 //

Fig. 5(C)

	9	18	27	36	45	54												
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	63		72		81			90			99			108				
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	117		126		135			144			153			162				
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	171		180		189			198			207			216				
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	225		234		243			252			261			270				
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	279		288		297			306			315			324				
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	333		342		351			360			369			378				
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	387		396		405			414			423			432				
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	441		450		459			468			477			486				
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	495		504		513			522			531			540				
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	549		558		567			576			585			594				
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

Fig. 5(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC ACC CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG					
-----	-----	-----	-----	-----	-----
E G S G G L K I A A F N I Q T F G E					
819	828	837	846	855	864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC					
-----	-----	-----	-----	-----	-----
T K M S N A T L V S Y I V Q I L S R					
873	882	891	900	909	918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG					
-----	-----	-----	-----	-----	-----
Y D I A L V Q E V R D S H L T A V G					
927	936	945	954	963	972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC					
-----	-----	-----	-----	-----	-----
K L L D N L N Q D A P D T Y H Y V V					
981	990	999	1008	1017	1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG					
-----	-----	-----	-----	-----	-----
S E P L G R N S Y K E R Y L F V Y R					
1035	1044	1053	1062	1071	1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC					
-----	-----	-----	-----	-----	-----
P D Q V S A V D S Y Y Y D D G C E P					
1089	1098	1107	1116	1125	1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG					
-----	-----	-----	-----	-----	-----
C G N D T F N R E P A I V R F F S R					
1143	1152	1161	1170	1179	1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC					
-----	-----	-----	-----	-----	-----
F T E V R E F A I V P L H A A P G D					
1197	1206	1215	1224	1233	1242

Fig. 5(D)
(Sheet 2 of 3)

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA

 A V A E I D A L Y D V Y L D V Q E K
 1251 1260 1269 1278 1287 1296
 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT

 W G L E D V M L M G D F N A G C S Y
 1305 1314 1323 1332 1341 1350
 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG

 V R P S Q W S S I R L W T S P T F Q
 1359 1368 1377 1386 1395 1404
 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT

 W L I P D S A D T T A T P T H C A Y
 1413 1422 1431 1440 1449 1458
 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG

 D R I V V A G M L L R G A V V P D S
 1467 1476 1485 1494 1503 1512
 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA

 A L P F N F Q A A Y G L S D Q L A Q
 1521 1530 1539 1548
 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 A I S D H Y P V E V M L K *

Fig. 5(D)
(Sheet 3 of 3)

pAS27

LOCUS PAS27.DNA 1584 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS (construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 446 g 310 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAG **GGAGCGGGCGG** GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTG
1021 TACAGGCCTG ACCAGGTGTC TGCAGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGGCC
1081 TGCAGGAAACG ACACCTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA
1141 GAGGTCAAGGG AGTTGCCAT TGTTCCCTG CATGCCGCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCAGGTGGAC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTG CCGACTCGGC TCTCCCTT AACTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA **GGGGGGCGGA**
1561 **CCCCAAAAAGA AGCGCAAGGT TTGA**

//

Fig. 6(A)

12 13 14

LOCUS FDDNASE27_ 1584 BP SS-DNA SYN 25-AUG-2000
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 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<787..1584)
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 frag 721..786
 /note="1 to 66 of 23/27linker"
 frag join(721..>735,<736..786)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 354 A 472 C 447 G 311 T 0 OTHER
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
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 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTAGATACAAAT
 241 GAGAAGTTCA AGGGCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAAGGG GGAGCGCGG GCTGAAGATC
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 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
 901 CACCTGACTG CCGTGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTG
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 1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCAACA
 1141 GAGGTCAGGG AGTTGCCAT TGTTCCCTG CATGGGCC CGGGGGACGC AGTAGCCGAG
 1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGCTT GGAGGACGTC
 1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
 1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
 1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
 1441 GCCGTTGTTG CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
 1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GGGGGGCGGA
 1561 CCCCCCAGA AGCGCAAGGT TTGA

//

Fig. 6(B)

LOCUS FDDNASE27K 1593 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<796..1593)
 /note="1 to 1584 of 27.dna [Split]"
 frag 730..795
 /note="1 to 66 of 23/27linker"
 frag join(730..>744,<745..795)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 478 C 449 G 311 T 0 OTHER
 ORIGIN -
 1 GCGGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT A CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTCC CCGAACCGGT GACGGTGTG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGGGTG CACACCTTC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGC
 781 CTGAAGATCG CAGCCTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 901 AGAGACAGCC ACCTGACTGC CGTGGGGAGA CTGCTGGACA ACCTCAATCA GGACGCACCA
 961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
 1021 CTGTCGTGT ACAGGCCTGA CCAGGTGTCT CGGGTGGACA GCTACTACTA CGATGATGGC
 1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
 1141 CGGTTCACAG AGGTCAAGGG A GTTGCCTATT GTTCCCCTGC ATGCGCCCC GGGGGACGCA
 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT CGGGGCTGCA GCTATGTGAG ACCCTCCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
 1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTA ACTTCCAGGC TGCCTATGGC
 1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 1561 GGGGCGGAC CCAAAAAGAA GCGCAAGGTT TGA

//

Fig. 6(C)

54

9	18	27	36	45	54
5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC					
-----	-----	-----	-----	-----	-----
M G W S C I I L F L V A T A T G V H					
-----	-----	-----	-----	-----	-----
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
-----	-----	-----	-----	-----	-----
S Q V Q L V Q S G A E V K K P G A S					
-----	-----	-----	-----	-----	-----
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
-----	-----	-----	-----	-----	-----
V K V S C K A S G Y T F S A Y W I E					
-----	-----	-----	-----	-----	-----
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
-----	-----	-----	-----	-----	-----
W V R Q A P G K G L E W V G E I L P					
-----	-----	-----	-----	-----	-----
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
-----	-----	-----	-----	-----	-----
G S N N S R Y N E K F K G R V T V T					
-----	-----	-----	-----	-----	-----
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
-----	-----	-----	-----	-----	-----
R D T S T N T A Y M E L S S L R S E					
-----	-----	-----	-----	-----	-----
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
-----	-----	-----	-----	-----	-----
D T A V Y Y C A R S Y D F A W F A Y					
-----	-----	-----	-----	-----	-----
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
-----	-----	-----	-----	-----	-----
W G Q G T L V T V S S A S T K G P S					
-----	-----	-----	-----	-----	-----
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
-----	-----	-----	-----	-----	-----
V F P L A P S S K S T S G G T A A L					
-----	-----	-----	-----	-----	-----
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
-----	-----	-----	-----	-----	-----
G C L V K D Y F P E P V T V S W N S					
-----	-----	-----	-----	-----	-----
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
-----	-----	-----	-----	-----	-----
G A L T S G V H T F P A V L Q S S G					

Fig. 6(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
---	---	---	---	---	---
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
---	---	---	---	---	---
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
---	---	---	---	---	---
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG					
---	---	---	---	---	---
E G S G G L K I A A F N I Q T F G E					
819	828	837	846	855	864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC					
---	---	---	---	---	---
T K M S N A T L V S Y I V Q I L S R					
873	882	891	900	909	918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG					
---	---	---	---	---	---
Y D I A L V Q E V R D S H L T A V G					
927	936	945	954	963	972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC					
---	---	---	---	---	---
K L L D N L N Q D A P D T Y H Y V V					
981	990	999	1008	1017	1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG					
---	---	---	---	---	---
S E P L G R N S Y K E R Y L F V Y R					
1035	1044	1053	1062	1071	1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC					
---	---	---	---	---	---
P D Q V S A V D S Y Y Y D D G C E P					
1089	1098	1107	1116	1125	1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG					
---	---	---	---	---	---
C G N D T F N R E P A I V R F F S R					
1143	1152	1161	1170	1179	1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC					
---	---	---	---	---	---
F T E V R E F A I V P L H A A P G D					
1197	1206	1215	1224	1233	1242

Fig. 6(D)
(Sheet 2 of 3)

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA

 A V A E I D A L Y D V Y L D V Q E K
 1251 1260 1269 1278 1287 1296
 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT

 W G L E D V M L M G D F N A G C S Y
 1305 1314 1323 1332 1341 1350
 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG

 V R P S Q W S S I R L W T S P T F Q
 1359 1368 1377 1386 1395 1404
 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT

 W L I P D S A D T T A T P T H C A Y
 1413 1422 1431 1440 1449 1458
 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG

 D R I V V A G M L L R G A V V P D S
 1467 1476 1485 1494 1503 1512
 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA

 A L P F N F Q A A Y G L S D Q L A Q
 1521 1530 1539 1548 1557 1566
 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA

 A I S D H Y P V E V M L K G G G P K
 1575 1584
 AAG AAG CGC AAG GTT TGA 3'

K K R K V *

Fig. 6D
(Sheet 3 of 3)

pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34
DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file)
REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS79 and AS80
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
SITES Note
BASE COUNT 501 a 677 c 607 g 411 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGGTGC CCAAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCCCA GCACCTGAAC TCCCTGGGGGG ACCGTCACTC
781 TTCCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGGTCT CCAACAAAGC CCTCCCAGGC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCCTCA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CTCCGGGTA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTC GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACCTGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAAGG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTC
1741 AACCGAGAGC CAGCCATTGT CAGGTTCTC TCCCGGTTCA CAGAGGTCAAG GGAGTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

//

Fig. 7(A)

5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	9	18	27	36	45	54												
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	63	72	81	90	99	108												
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	117	126	135	144	153	162												
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	171	180	189	198	207	216												
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	225	234	243	252	261	270												
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	279	288	297	306	315	324												
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	333	342	351	360	369	378												
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	387	396	405	414	423	432												
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	441	450	459	468	477	486												
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	495	504	513	522	531	540												
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	549	558	567	576	585	594												
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G
	603	612	621	630	639	648												
	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
	657	666	675	684	693	702												

Fig. 7(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

Fig. 7(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404												
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	GGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K	<u>G</u>
1413	1422	1431	1440	1449	1458												
AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
<u>S</u>	<u>G</u>	<u>G</u>	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K
1467	1476	1485	1494	1503	1512												
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D
1521	1530	1539	1548	1557	1566												
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L
1575	1584	1593	1602	1611	1620												
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E
1629	1638	1647	1656	1665	1674												
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D
1683	1692	1701	1710	1719	1728												
CAG	GTG	TCT	GCG	GTG	GAC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG	
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G
1737	1746	1755	1764	1773	1782												
AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T
1791	1800	1809	1818	1827	1836												
GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V
1845	1854	1863	1872	1881	1890												
GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GCG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G
1899	1908	1917	1926	1935	1944												
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R
1953	1962	1971	1980	1989	1998												
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L
2007	2016	2025	2034	2043	2052												
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R

Fig. 7(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106																		
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT						
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L						
2115	2124	2133	2142	2151	2160	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I						
2169	2178	2187	2196			AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'					
-	-	-	-	-	-	S	D	H	Y	P	V	E	V	M	L	K	*						

Fig. 7(B)
(Sheet 4 of 4)

pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35
DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)
REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS81 and AS82
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
SITES Note
BASE COUNT 500 a 677 c 606 g 410 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACACTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTGCTCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCAC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTC CCCGAACCGG TGACGGTGTG TGGAACTCA
541 GGCGCCCTGA CCAGGGCGT GCACACCTTC CGGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGA CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTG
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
841 TCGCTGGTGG TGGACGTGAG CCACGAAGAC CTCAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCAGGCC CCCATCGAGA AAACCATCTC CAAAGCCAA
1081 GGGCAGCCCC GAGAACCCACA GGTGTACACC CTGCCCCAT CCCGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAA GGCTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGAGGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CTCCGAAg~~GG~~ GAGCGCCGAG CTGAAGATCG CAGCCTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTG AGAGACAGCC ACCTGACTGC CGTGGGGAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGGACCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAAGGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGCCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

//

Fig. 8(A)

5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	63		72		81		90		99		108							
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	117		126		135		144		153		162							
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	171		180		189		198		207		216							
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	225		234		243		252		261		270							
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	279		288		297		306		315		324							
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	333		342		351		360		369		378							
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	387		396		405		414		423		432							
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	441		450		459		468		477		486							
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	495		504		513		522		531		540							
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTC	AGC	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	549		558		567		576		585		594							
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G
	603		612		621		630		639		648							
	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
	657		666		675		684		693		702							

Fig. 8(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

Fig. 8(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC					
A L H N H Y T Q K S L S L S P K <u>G</u> S					
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG					
<u>G</u> G L K I A A F N I Q T F G E T K M					
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC					
S N A T L V S Y I V Q I L S R Y D I					
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG					
A L V Q E V R D S H L T A V G K L L					
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA					
D N L N Q D A P D T Y H Y V V S E P					
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG					
L G R N S Y K E R Y L F V Y R P D Q					
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC					
V S A V D S Y Y D D G C E P C G N					
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG					
D T F N R E P A I V R F F S R F T E					
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC					
V R E F A I V P L H A A P G D A V A					
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG					
E I D A L Y D V Y L D V Q E K W G L					
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC					
E D V M L M G D F N A G C S Y V R P					
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC					
S Q W S S I R L W T S P T F Q W L I					
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC					
P D S A D T T A T P T H C A Y D R I					

Fig. 8(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC					
-----	-----	-----	-----	-----	-----
V V A G M L L R G A V V P D S A L P					
2115	2124	2133	2142	2151	2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT					
-----	-----	-----	-----	-----	-----
F N F Q A A Y G L S D Q L A Q A I S					
2169	2178	2187			
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'					
-----	-----	-----	-----	-----	-----
D H Y P V E V M L K *					

Fig. 8(B)
(Sheet 4 of 4)

pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998

DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36

DEFINITION Clone 18.24.1 with residue 1392 T > C

REFERENCE

 AUTHORS VERHOEYEN ET AL

 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc

 JOURNAL IMMUNOL. (1993):78, 364-370

COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)

COMMENT The fusion was made using overlapping oligos AS83 and AS84

FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)

FEATURES Residue 963 is G > T leading to silent mutation in all clones

FEATURES Residue 1392 T > C silent S to S mutation

SITES Note

BASE COUNT 498 a 678 c 605 g 409 t

ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGCCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCACTG
781 TTCCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCTCCTAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCCACA GGTGTACACC CTGGCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CccCGGGAG CGGGCGGGCTG AAGATCGCAG CCTTCACAT CCAGACATT
1441 GGGGAGACCA AGATGTCCAA TGCCACCTC GTCACTACA TTGTGAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAAACC TCAATCAGGA CGCACAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTGCTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACCGAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTGGAG GACGTCTGT TGATGGCGA CTTCAATGCG
1921 GGCTGAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGAACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 9(A)

9 18 27 36 45 54
 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTC GCA GCA ACA GCT ACA GGT GTC GAC
 M G W S C I I L F L V A T A T G V H
 63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
 S Q V Q L V Q S G A E V K K P G A S
 117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
 V K V S C K A S G Y T F S A Y W I E
 171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
 W V R Q A P G K G L E W V G E I L P
 225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
 G S N N S R Y N E K F K G R V T V T
 279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
 R D T S T N T A Y M E L S S L R S E
 333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
 D T A V Y Y C A R S Y D F A W F A Y
 387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
 W G Q G T L V T V S S A S T K G P S
 441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
 V F P L A P S S K S T S G G T A A L
 495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG AGC GTG TCG TGG AAC TCA
 G C L V K D Y F P E P V T V S W N S
 549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
 G A L T S G V H T F P A V L Q S S G
 603 612 621 630 639 648
 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
 L Y S L S S V V T V P S S S L G T Q
 657 666 675 684 693 702

Fig. 9(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

Fig. 9(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC					
-----	-----	-----	-----	-----	-----
A L H N H Y T Q K S L S L S P G S G					
1413	1422	1431	1440	1449	1458
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC					
-----	-----	-----	-----	-----	-----
<u>G</u> L K I A A F N I Q T F G E T K M S					
1467	1476	1485	1494	1503	1512
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC					
-----	-----	-----	-----	-----	-----
N A T L V S Y I V Q I L S R Y D I A					
1521	1530	1539	1548	1557	1566
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC					
-----	-----	-----	-----	-----	-----
L V Q E V R D S H L T A V G K L L D					
1575	1584	1593	1602	1611	1620
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG					
-----	-----	-----	-----	-----	-----
N L N Q D A P D T Y H Y V V S E P L					
1629	1638	1647	1656	1665	1674
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG					
-----	-----	-----	-----	-----	-----
G R N S Y K E R Y L F V Y R P D Q V					
1683	1692	1701	1710	1719	1728
TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC					
-----	-----	-----	-----	-----	-----
S A V D S Y Y D D G C E P C G N D					
1737	1746	1755	1764	1773	1782
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC					
-----	-----	-----	-----	-----	-----
T F N R E P A I V R F F S R F T E V					
1791	1800	1809	1818	1827	1836
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG					
-----	-----	-----	-----	-----	-----
R E F A I V P L H A A P G D A V A E					
1845	1854	1863	1872	1881	1890
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG					
-----	-----	-----	-----	-----	-----
I D A L Y D V Y L D V Q E K W G L E					
1899	1908	1917	1926	1935	1944
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC					
-----	-----	-----	-----	-----	-----
D V M L M G D F N A G C S Y V R P S					
1953	1962	1971	1980	1989	1998
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC					
-----	-----	-----	-----	-----	-----
Q W S S I R L W T S P T F Q W L I P					
2007	2016	2025	2034	2043	2052
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG					
-----	-----	-----	-----	-----	-----
D S A D T T A T P T H C A Y D R I V					

Fig. 9(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106												
GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC	TTT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L	P	F
2115	2124	2133	2142	2151	2160												
AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I	S	D
2169	2178	2187															
CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'							
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
H	Y	P	V	E	V	M	L	K	*								

Fig. 9(B)
(Sheet 4 of 4)

pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-
1998

DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37

DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file) plus NLS

REFERENCE

AUTHORS VERHOEYEN ET AL

TITLE CONSTRUCTION OF RESHAPED HMFG1 etc

JOURNAL IMMUNOL. (1993):78, 364-370

COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)

COMMENT The fusion was made using overlapping oligos AS79 and AS80

FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)

FEATURES Residue 963 is G > T leading to silent mutation in all clones

SITES Note

BASE COUNT 511 a 683 c 619 g 413 t

ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGG ACCGTCAGTC
781 TTCCCTTCTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCAGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGAGGCC GGAGAACAC TACAAGACCA CGCCTCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCCTCA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGAC
1381 CTCTCCCTGT CTCCGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCTG
1501 AGCCGCTACG ACATGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGAA CGACACCTC
1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCAGTTCA CAGAGGTGAG GGAGTTGCCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGAGC TCATGTTGAT GGGCAGCTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCCTCC CAGTGGTCAT CCATCCGCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACG GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACAT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCAAAAAA GAAGCGCAAG
2221 GTTTGA

//

→ NLS

Fig. 10(A)

9	18	27	36	45	54												
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H

63 72 81 90 99 108																	
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S

117 126 135 144 153 162																	
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E

171 180 189 198 207 216																	
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P

225 234 243 252 261 270																	
GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T

279 288 297 306 315 324																	
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E

333 342 351 360 369 378																	
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TPT	GCT	TAC
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y

387 396 405 414 423 432																	
TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S

441 450 459 468 477 486																	
GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L

495 504 513 522 531 540																	
GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S

549 558 567 576 585 594																	
GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

603 612 621 630 639 648																	
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q

657 666 675 684 693 702																	

Fig. 10(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CCG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC AGC TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

Fig. 10(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG					
A L H N H Y T Q K S L S L S P G K <u>G</u>					
1413	1422	1431	1440	1449	1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
<u>S</u> G G L K I A A F N I Q T F G E T K					
1467	1476	1485	1494	1503	1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
M S N A T L V S Y I V Q I L S R Y D					
1521	1530	1539	1548	1557	1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
I A L V Q E V R D S H L T A V G K L					
1575	1584	1593	1602	1611	1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
L D N L N Q D A P D T Y H Y V V S E					
1629	1638	1647	1656	1665	1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
P L G R N S Y K E R Y L F V Y R P D					
1683	1692	1701	1710	1719	1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
Q V S A V D S Y Y D D G C E P C G					
1737	1746	1755	1764	1773	1782
AAC GAC ACC TTC AAC CGA GAG CCA ATT GTC AGG TTC TTC TCC CGG TTC ACA					
N D T F N R E P A I V R F F S R F T					
1791	1800	1809	1818	1827	1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
E V R E F A I V P L H A A P G D A V					
1845	1854	1863	1872	1881	1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC					
A E I D A L Y D V Y L D V Q E K W G					
1899	1908	1917	1926	1935	1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA					
L E D V M L M G D F N A G C S Y V R					
1953	1962	1971	1980	1989	1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG					
P S Q W S S I R L W T S P T F Q W L					
2007	2016	2025	2034	2043	2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG					
I P D S A D T T A T P T H C A Y D R					

Fig. 10(B)
(Sheet 3 of 4)

2061 2070 2079 2088 2097 2106
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
 - - - - -
 I V V A G M L L R G A V V P D S A L

 2115 2124 2133 2142 2151 2160
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
 - - - - -
 P F N F Q A A Y G L S D Q L A Q A I

 2169 2178 2187 2196 2205 2214
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG
 - - - - -
 S D H Y P V E V M L K G G G P K K K

 2223
 CGC AAG GTT TGA 3'
 - - - - -
R K V *

Fig. 10(B)
(Sheet 4 of 4)

pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38
DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS81 and AS82
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
SITES Note
BASE COUNT 510 a 683 c 618 g 412 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TCGAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCTTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCCA ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCCTCTTC CCCCCAAACC CAAGGACACC CTCATGATCT CCGGACCCCC TGAGGTACCA
841 TGGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCAGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TCGAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCCACA GGTGTACACC CTGCCCCCAT CCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGAGGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
1261 GACGGCTCTT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGG GAGCGGGCGGG CTGAAGATCG CAGCCTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTG AGAGACAGCC ACCTGACTGC CGTGGGAAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGT ACAGGCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT CGGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCCTGC ATGCGGCCCG GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCG
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CGGTTGTTCC CGACTCGGCT
2101 CTTCCCCCTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGCGGAC CCAAAAGAA GCGCAAGGTT

2221 TGA

→ NLS

Fig. 11(A)

5'

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
-----	-----	-----	-----	-----	-----
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
-----	-----	-----	-----	-----	-----
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
-----	-----	-----	-----	-----	-----
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
-----	-----	-----	-----	-----	-----
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
-----	-----	-----	-----	-----	-----
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
-----	-----	-----	-----	-----	-----
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
-----	-----	-----	-----	-----	-----
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
-----	-----	-----	-----	-----	-----
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
-----	-----	-----	-----	-----	-----
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
-----	-----	-----	-----	-----	-----
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
-----	-----	-----	-----	-----	-----
G A L T S G V H T F P A V L Q S S G					
603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702

Fig. 11(B)
(Sheet 1 of 4)

ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K	
711	720	729	738	747	756													
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P	
765	774	783	792	801	810													
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
E	L	L	G	G	P	S	V	F	L	F	P	P	P	K	P	K	D	T
819	828	837	846	855	864													
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H	
873	882	891	900	909	918													
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N	
927	936	945	954	963	972													
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	
981	990	999	1008	1017	1026													
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	
1035	1044	1053	1062	1071	1080													
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K	
1089	1098	1107	1116	1125	1134													
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L	
1143	1152	1161	1170	1179	1188													
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC		
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	
1197	1206	1215	1224	1233	1242													
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T	
1251	1260	1269	1278	1287	1296													
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V	
1305	1314	1323	1332	1341	1350													
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E	

Fig. 11(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC					
A L H N H Y T Q K S L S L S P K G S					
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG					
<u>G</u> G L K I A A F N I Q T F G E T K M					
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC					
S N A T L V S Y I V Q I L S R Y D I					
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG					
A L V Q E V R D S H L T A V G K L L					
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA					
D N L N Q D A P D T Y H Y V V S E P					
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG					
L G R N S Y K E R Y L F V Y R P D Q					
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC					
V S A V D S Y Y D D G C E P C G N					
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG					
D T F N R E P A I V R F F S R F T E					
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC					
V R E F A I V P L H A A P G D A V A					
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG					
E I D A L Y D V Y L D V Q E K W G L					
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC					
E D V M L M G D F N A G C S Y V R P					
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC					
S Q W S S I R L W T S P T F Q W L I					
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACC CAC TGT GCC TAT GAC AGG ATC					
P D S A D T T A T P T H C A Y D R I					

Fig. 11(C)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC					
---	---	---	---	---	---
V V A G M L L R G A V V P D S A L P					
2115	2124	2133	2142	2151	2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT					
---	---	---	---	---	---
F N F Q A A Y G L S D Q L A Q A I S					
2169	2178	2187	2196	2205	2214
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC					
---	---	---	---	---	---
D H Y P V E V M L K G G G P K K K R					
2223					
AAG GTT TGA 3'					
---	---	---	---	---	---
K V *					
=====					

Fig. 11(D)
(Sheet 4 of 4)

pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-
1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39
DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS83 and AS84
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES Residue 1392 T > C silent S to S mutation
SITES Note
BASE COUNT 508 a 684 c 617 g 411 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACCTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTGCTCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGC CGTCCCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCACTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGGCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCTTCAC CGTCTGAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGAGGCC GGAGAACAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CcCGGGGAG GGCGGGCTG AAGATCGCAG CCTCTAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCTA TGCCACCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TAGGACATCG CCCTGGTCCA GGAGGTAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAAACC TCAATCAGGA CGCACAGAC ACCTATCAGT ACCTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACCCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTGGAG GACGTCTAGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGAGG GATGCTGCTC CGAGGGGCCG TTGTTCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGGG GGCGGACCCA AAAAGAACG CAAGGTTGA

//

Fig. 12(A)

9 18 27 36 45 54
 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

 M G W S C I I L F L V A T A T G V H
 63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

 S Q V Q L V Q S G A E V K K P G A S
 117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

 V K V S C K A S G Y T F S A Y W I E
 171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

 W V R Q A P G K G L E W V G E I L P
 225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

 G S N N S R Y N E K F K G R V T V T
 279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

 R D T S T N T A Y M E L S S L R S E
 333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

 D T A V Y Y C A R S Y D F A W F A Y
 387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

 W G Q G T L V T V S S A S T K G P S
 441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

 V F P L A P S S K S T S G G T A A L
 495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

 G C L V K D Y F P E P V T V S W N S
 549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

 G A L T S G V H T F P A V L Q S S G
 603 612 621 630 639 648
 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

 L Y S L S S V V T V P S S S L G T Q
 657 666 675 684 693 702

Fig. 12(B)
(Sheet 1 of 4)

ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T
819	828	837	846	855	864												
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H
873	882	891	900	909	918												
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N
927	936	945	954	963	972												
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S
981	990	999	1008	1017	1026												
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GCC	AAG	GAG	TAC	AAG	TGC	AAG
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K
1035	1044	1053	1062	1071	1080												
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K
1089	1098	1107	1116	1125	1134												
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L
1143	1152	1161	1170	1179	1188												
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D
1197	1206	1215	1224	1233	1242												
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T
1251	1260	1269	1278	1287	1296												
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V
1305	1314	1323	1332	1341	1350												
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E

Fig. 12(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404												
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCC	CCG	GGG	AGC	GGC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	<u>G</u>	<u>S</u>	<u>G</u>
1413	1422	1431	1440	1449	1458												
GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG	ATG	TCC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
<u>G</u>	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K	M	S
1467	1476	1485	1494	1503	1512												
AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC	ATC	GCC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D	I	A
1521	1530	1539	1548	1557	1566												
CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG	CTG	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L	L	D
1575	1584	1593	1602	1611	1620												
AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG	CCA	CTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E	P	L
1629	1638	1647	1656	1665	1674												
GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC	CAG	GTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D	Q	V
1683	1692	1701	1710	1719	1728												
TCT	GGC	GTG	GAC	AGC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG	AAC	GAC	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
S	A	V	D	S	Y	Y	D	D	G	C	E	P	C	G	N	D	
1737	1746	1755	1764	1773	1782												
ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA	GAG	GTC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T	E	V
1791	1800	1809	1818	1827	1836												
AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA	GCC	GAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V	A	E
1845	1854	1863	1872	1881	1890												
ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GGC	TTG	GAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G	L	E
1899	1908	1917	1926	1935	1944												
GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA	CCC	TCC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R	P	S
1953	1962	1971	1980	1989	1998												
CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG	ATC	CCC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L	I	P
2007	2016	2025	2034	2043	2052												
GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG	ATC	GTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R	I	V

Fig. 12(B)
(Sheet 3 of 4)

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pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASe1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 343 a 467 c 430 g 308 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTC CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
541 GGCGCCCTGA CCAGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGCAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAG CGGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTGAG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTCGGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACAGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCC CCGAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGG TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Fig. 13(A)

LOCUS FDDNASE101 1548 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<781..1548)
 /note="1 to 1548 of PAS101.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 343 A 465 C 431 G 309 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTCCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCAT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAACACTA
 541 GGCGCCCTGA CCAGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTGGA GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAAGGTTCT TCTCCCGTT CACAGAGGTC
 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCC CCGAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Fig. 13(B)

LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1557
 /note="1 to 1548 of FdDNase101correct"
 frag join(10..>729,<790..1557)
 /note="1 to 1548 of PAS101.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTGC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCACAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCACAT GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGACACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGT CACACCTTC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGAAC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CGTGTCCAG CACCAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCCTCGTC
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAAGAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTC
 1021 GTGTACAGGC CTGACCAGGT GTCTGCGGT GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCAGGGAA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
 1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGGAC
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCACTATG TGAGACCCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACCGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACAC TATCCAGTGG AGGTGATGCT GAAGTGA

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Fig. 13(C)

	9	18	27	36	45	54
5'	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					

Fig. 13(D)
(Sheet 1 of 3)

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
E	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K
819	828	837	846	855	864												
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D
873	882	891	900	909	918												
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L
927	936	945	954	963	972												
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E
981	990	999	1008	1017	1026												
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D
1035	1044	1053	1062	1071	1080												
CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G
1089	1098	1107	1116	1125	1134												
AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T
1143	1152	1161	1170	1179	1188												
GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V
1197	1206	1215	1224	1233	1242												

Fig. 13(D)
(Sheet 2 of 3)

GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GGC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G
1251	1260	1269	1278	1287	1296												
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GGC	GGC	TGC	AGC	TAT	GTG	AGA
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R
1305	1314	1323	1332	1341	1350												
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L
1359	1368	1377	1386	1395	1404												
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R
1413	1422	1431	1440	1449	1458												
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L
1467	1476	1485	1494	1503	1512												
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I
1521	1530	1539	1548														
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
S	D	H	Y	P	V	E	V	M	L	K	*						

Fig. 13(D)
(Sheet 3 of 3)

pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna) (See Figure 2)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 345 a 469 c 440 g 312 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAACCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTAGATAACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCTG **TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC**
781 **GGG**CTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACCTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCA GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
1321 CAGTGGTCAT CCATCCGCT GTGGACAAGC CCCACCTTC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GCCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA

//

Fig. 14(A)

LOCUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER
 ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCAC AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACTCA
 541 GCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTC AGCAGCTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGGGTGG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCCTGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCC TGCACTGGGC CCCGGGGGAC
 1201 GCAGTAGCCG AGATGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTC AGTGGCTGAT CCCCGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAAGGGATG
 1441 CTGCTCCGAG GGGCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTCCA GGCTGCCTAT
 1501 GGCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
 1561 AAGTGA

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Fig. 14(B)

pAS302

LOCUS	FDDNASE302	1575	BP	SS-DNA	SYN	29-AUG-2000				
DEFINITION	-									
ACCESSION	-									
KEYWORDS	-									
SOURCE	-									
FEATURES		Location/Qualifiers								
frag		10..1575								
		/note="1 to 1566 of FdDNase102correct"								
BASE COUNT	346	A	474	C	442	G	313	T	0	OTHER
ORIGIN	-									
1	GCCGCCACCA	TGGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTGTC				
61	CACTCCCAGG	TGCAGCTGGT	GCAGTCTGGG	GCAGAGGTGA	AAAAGCCTGG	GGCCTCAGTG				
121	AAGGTGTCT	GCAAGGCTTC	TGGCTACACC	TTCACTGCCT	ACTGGATAGA	GTGGGTGCGC				
181	CAGGCTCCAG	GAAAGGGCCT	CGAGTGGGTC	GGAGAGATT	TACCTGGAAG	TAATAATTCT				
241	AGATACAATG	AGAAGTTCAA	GGGCGGAGTG	ACAGTCACTA	GAGACACATC	CACAAACACA				
301	GCCTACATGG	AGCTCAGCAG	CCTGAGGTCT	GAGGACACAG	CCGTCTATTA	CTGTGCAAGA				
361	TCCTACGACT	TTGCTCTGGTT	TGCTTACTGG	GGCCAAGGGG	CTCTGGTCAC	AGTCTCTCA				
421	GCCTCCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCC	CCTCCAAGAG	CACCTCTGGG				
481	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTGCG				
541	TGGAACTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA				
601	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC				
661	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGTTGAGCCC				
721	AAATCTTGTG	ACAAAACCTCA	CACATGCTGT	GTCGAGTGTC	CACCGTGTCC	AGCACCAGAG				
781	GGGAGCGGGG	GGCTGAAGAT	CGCAGCCTTC	AACATCCAGA	CATTTGGGA	GACCAAGATG				
841	TCCAATGCCA	CCCTCGTCAG	CTACATTGTG	CAGATCCTGA	GCCGCTACGA	CATGCCCTG				
901	GTCCAGGAGG	TCAGAGACAG	CCACCTGACT	GCCGTGGGG	AGCTGCTGGA	CAACCTCAAT				
961	CAGGACGCAC	CAGACACCTA	TCACTACGTG	GTCAGTGAGC	CACTGGGACG	GAACAGCTAT				
1021	AAGGAGCGCT	ACCTGTTCGT	GTACAGGCCT	GACCAGGTGT	CTGCGGTGGA	CAGCTACTAC				
1081	TACGATGATG	GCTGGAGGCC	CTGCGGGAAC	GACACCTCA	ACCGAGAGCC	AGCCATTGTC				
1141	AGGTTCTTCT	CCCGGTTCAC	AGAGGTCAGG	GAGTTTGCCA	TTGTTCCCT	GCATGCGGCC				
1201	CCGGGGGACG	CAGTAGCCGA	GATCGACGCT	CTCTATGACG	TCTACCTGGA	TGTCCAAGAG				
1261	AAATGGGGCT	TGGAGGACGT	CATGTTGATG	GGCGACTTCA	ATGCGGGCTG	CAGCTATGTG				
1321	AGACCCCTCC	AGTGGTCATC	CATCCGCTG	TGGACAAGCC	CCACCTTCCA	GTGGCTGATC				
1381	CCCGACAGCG	CTGACACCC	AGCTACACCC	ACGCACGTG	CCTATGACAG	GATCGTGGTT				
1441	GCAGGGATGC	TGCTCCGAGG	GGCCGTTGTT	CCCGACTCGG	CTCTTCCCTT	TAACCTCCAG				
1501	GCTGCCTATG	GCCTGAGTGA	CCAATGGCC	CAAGCCATCA	GTGACCACTA	TCCAGTGGAG				
1561	GTGATGCTGA	AGTGA								

//

Fig. 14(C)

54

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					

Fig. 14(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG					
-----	-----	-----	-----	-----	-----
C P A P E G S G G L K I A A F N I Q					
819	828	837	846	855	864
ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG					
-----	-----	-----	-----	-----	-----
T F G E T K M S N A T L V S Y I V Q					
873	882	891	900	909	918
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG					
-----	-----	-----	-----	-----	-----
I L S R Y D I A L V Q E V R D S H L					
927	936	945	954	963	972
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT					
-----	-----	-----	-----	-----	-----
T A V G K L L D N L N Q D A P D T Y					
981	990	999	1008	1017	1026
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG					
-----	-----	-----	-----	-----	-----
H Y V V S E P L G R N S Y K E R Y L					
1035	1044	1053	1062	1071	1080
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT					
-----	-----	-----	-----	-----	-----
F V Y R P D Q V S A V D S Y Y Y D D					
1089	1098	1107	1116	1125	1134
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG					
-----	-----	-----	-----	-----	-----
G C E P C G N D T F N R E P A I V R					
1143	1152	1161	1170	1179	1188
TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG					
-----	-----	-----	-----	-----	-----
F F S R F T E V R E F A I V P L H A					
1197	1206	1215	1224	1233	1242

Fig. 14(D)
(Sheet 2 of 3)

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT

 A P G D A V A E I D A L Y D V Y L D
 1251 1260 1269 1278 1287 1296
 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG

 V Q E K W G L E D V M L M G D F N A
 1305 1314 1323 1332 1341 1350
 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC

 G C S Y V R P S Q W S S I R L W T S
 1359 1368 1377 1386 1395 1404
 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG

 P T F Q W L I P D S A D T T A T P T
 1413 1422 1431 1440 1449 1458
 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT

 H C A Y D R I V V A G M L L R G A V
 1467 1476 1485 1494 1503 1512
 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC

 V P D S A L P F N F Q A A Y G L S D
 1521 1530 1539 1548 1557 1566
 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 Q L A Q A I S D H Y P V E V M L K *

Fig. 14(D)
(Sheet 3 of 3)

pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 436 g 312 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACCTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
361 TTGCTCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATCTC ACACATGCTG **TGTGGAGTG** **CCACCGT**GCC **CAGCACCTGA** **AGGC**GGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCCCTC
841 GTCAGCTACA TTGTGAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGAATGCCGT GGGGAAGCTG CTGGACAAACC TCAATCAGGA CGCACCAAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGGC GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCAATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGAACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 15(A)

LOCUS FDDNASE103 1560 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1560)
 /note="1 to 1560 of PAS103.dna [Split]"
 frag 721..792
 /note="1 to 72 of 103/107linker"
 frag join(721..>771,<772..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 344 A 467 C 436 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTGCTCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
 541 GGCCTCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATT GGGGAGACCA AGATGTCAA TGCCACCC
 841 GTCAGCTACA TTGTGCAAGAT CCTGAGCCGC TAGACATCG CCCTGGTCCA GGAGGTCAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCGTACCA GGTGTCTCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCC
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGGCCCCGGG GGACGCA
 1201 GCGCAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCACTGT TGATGGGCGA CTTCAATGCG GGTGCAAGCT ATGTGAGACC CTCCCCAGTGG
 1321 TCATCCATCC GCCTGTTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTCCCCGA CTCGGCTCTT CCCCTTAAC TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 15(B)

LOCUS FDDNASE103 1569 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<802..1569)
 /note="1 to 1560 of PAS103.dna [Split]"
 frag 730..801
 /note="1 to 72 of 103/107linker"
 frag join(730..>780,<781..801)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 473 C 438 G 313 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAACGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCACATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGGGCGTG CACACCTTCC CCGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTGAGTGTC CACCGTGTCC AGCACCAGAG
 781 GGCAGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTG GGGAGACCAA GATGTCCAAT
 841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
 901 GAGGTCAAGAG ACAGCCACCT GACTGCCGTG GGGAAAGCTGC TGGACAACCT CAATCAGGAC
 961 GCACCAAGACA CCTATCACTA CGTGGTCACT GAGCCACTGG GACGGAACAG CTATAAGGAG
 1021 CGCTACCTGT TCGTGTACAG GCCTGACAG GTGCTGCGG TGGACAGCTA CTACTACGAT
 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAAGGTT
 1141 TTCTCCCAGG TTCAACAGAGGT CAGGGAGTTT GCCATTGTT CCCTGCATGC GGCCCCGGGG
 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
 1261 GGCTTGGAGG ACGTCACTGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
 1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
 1381 AGCGCTGACA CCACAGCTAC ACCCACGAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
 1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACCT CCAGGCTGCC
 1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
 1561 CTGAAGTGA

//

Fig. 15(C)

9 18 27 36 45 54
 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC
 M G W S C I I L F L V A T A T G V H
 63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
 S Q V Q L V Q S G A E V K K P G A S
 117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
 V K V S C K A S G Y T F S A Y W I E
 171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
 W V R Q A P G K G L E W V G E I L P
 225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
 G S N N S R Y N E K F K G R V T V T
 279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
 R D T S T N T A Y M E L S S L R S E
 333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
 D T A V Y Y C A R S Y D F A W F A Y
 387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
 W G Q G T L V T V S S A S T K G P S
 441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
 V F P L A P S S K S T S G G T A A L
 495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
 G C L V K D Y F P E P V T V S W N S
 549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
 G A L T S G V H T F P A V L Q S S G

Fig. 15(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
-----	-----	-----	-----	-----	-----
C P A P E G G L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
-----	-----	-----	-----	-----	-----
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
-----	-----	-----	-----	-----	-----
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
-----	-----	-----	-----	-----	-----
V G K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
-----	-----	-----	-----	-----	-----
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC					
-----	-----	-----	-----	-----	-----
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
-----	-----	-----	-----	-----	-----
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
-----	-----	-----	-----	-----	-----
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

Fig. 15(D)
(Sheet 2 of 3)

X5
21

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA

 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC

 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC

 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT

 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC

 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG

 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 A Q A I S D H Y P V E V M L K *

Fig. 15(D)
(Sheet 3 of 3)

pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
Position 924 G to A by ggg to gag
Linker GR instead of GG (position 777)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 346 a 468 c 434 g 312 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG **TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG**
781 AAGATCGCAG CCTTCAACAT CCAGACATT GGGGAGACCA AGATGTCCAA TGCCACCCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TAGACATCG CCCTGGTCCA GGAGGTGAGA
901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGGC GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
1201 GCGGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTACCAAC TGGCCAAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 16(A)

LOCUS FDDNASE104 1560 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag 721..792
 /note="1 to 72 of 104linker"
 frag join(721..>774,<776..792)
 /note="1 to 72 of 103linker [Split]"
 frag join(721..>771,<772..>774,<776..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGGCT TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTC CCCGAACCGG TGACGGTGTG TGGAACACTA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCCCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
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 721 GACAAAACTC ACACATGCTG TGTGAGTGT CCACCGTGTG CAGCACCGAGA GGGCAGGCTG
 781 AAAGATCGCAG CCTTCAACAT CCAGACATT GGGGAGACCA AGATGTCCAA TGCCACCTC
 841 GTCAGCTACA TTGTGCAAGAT CCTGAGCCGC TAGGACATCG CCCTGGTCCA GGAGGTCA
 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCGAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCTGACCA GGTGTCTGGT GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGGCCCGGG GGACGCGAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCACTG TGATGGGCGA CCTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCATT GACAGGATCG TGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTCCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 16(B)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC

9 18 27 36 45 54.

M G W S C I I L F L V A T A T G W H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

Fig. 16(C)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
-----	-----	-----	-----	-----	-----
C P A P E G R L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
-----	-----	-----	-----	-----	-----
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
-----	-----	-----	-----	-----	-----
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
-----	-----	-----	-----	-----	-----
V E K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
-----	-----	-----	-----	-----	-----
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC					
-----	-----	-----	-----	-----	-----
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
-----	-----	-----	-----	-----	-----
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
-----	-----	-----	-----	-----	-----
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

Fig. 16(C)
(Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA

 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC

 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC

 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT

 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC

 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG

 D 'S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 A Q A I S D H Y P V E V M L K *

Fig. 16(C)
(Sheet 3 of 3)

pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS (pAS105)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 353 a 473 c 442 g 310 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGA CGTGCCTCC AGCAGCTTG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAG CGGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTGGA GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCAGA GCCCTGCAGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAAGGTTCT TCTCCGGTT CACAGAGGTC
1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCAA GAGAAATGGG GCTTGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGCAGCA CTATCCAGTG GAGGTGATGC TGAAGGGGG CGGACCCAAA
1561 **AAGAAGCGCA AGGTTTGA**

//

→ NLS

Fig. 17(A)

LOCUS FDDNASE105 1578 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<781..1578)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 353 A 471 C 443 G 311 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCACTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAAGGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTGAGG GGAGACCAAG ATGTCATG CCACCCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTCGGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGTT CACAGAGGTC
 1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCC CCGAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGG CGGACCCAAA
 1561 AAGAAGCGCA AGGTTTGA

//

Fig. 17(B)

LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1587
 /note="1 to 1578 of FdDNase105correct"
 frag join(10..>729,<790..1587)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
 361 TCCTACGACT TTGCTCTGGTT TGCTTACTGG GGCCAAGGGG CTCTGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTGGG GAGACCAAGA TGTCCAATGC CACCCCTCGTC
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGG CGGAACAGCT ATAAGGAGCG CTACCTGTC
 1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCGGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTT
 1141 ACAGAGGTCA GGGAGTTTG CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACCGACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCACT TATCCAGTGG AGGTGATGCT GAAGGGGGGC
 1561 GGACCCAAAA AGAACCGCAA GGTTTGA

//

Fig. 17(C)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

Fig. 17(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC ACC GTG CCC TCC AGC AGC TTG GGC ACC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
-----	-----	-----	-----	-----	-----
E G G L K I A A F N I Q T F G E T K					
819	828	837	846	855	864
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
-----	-----	-----	-----	-----	-----
M S N A T L V S Y I V Q I L S R Y D					
873	882	891	900	909	918
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
-----	-----	-----	-----	-----	-----
I A L V Q E V R D S H L T A V G K L					
927	936	945	954	963	972
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
-----	-----	-----	-----	-----	-----
L D N L N Q D A P D T Y H Y V V S E					
981	990	999	1008	1017	1026
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
-----	-----	-----	-----	-----	-----
P L G R N S Y K E R Y L F V Y R P D					
1035	1044	1053	1062	1071	1080
CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
-----	-----	-----	-----	-----	-----
Q V S A V D S Y Y D D G C E P C G					
1089	1098	1107	1116	1125	1134
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
-----	-----	-----	-----	-----	-----
N D T F N R E P A I V R F F S R F T					
1143	1152	1161	1170	1179	1188
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
-----	-----	-----	-----	-----	-----
E V R E F A I V P L H A A P G D A V					
1197	1206	1215	1224	1233	1242

Fig. 17(D)
(Sheet 2 of 3)

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC

 A E I D A L Y D V Y L D V Q E K W G
 1251 1260 1269 1278 1287 1296
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA

 L E D V M L M G D F N A G C S Y V R
 1305 1314 1323 1332 1341 1350
 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG

 P S Q W S S I R L W T S P T F Q W L
 1359 1368 1377 1386 1395 1404
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG

 I P D S A D T T A T P T H C A Y D R
 1413 1422 1431 1440 1449 1458
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

 I V V A G M L L R G A V V P D S A L
 1467 1476 1485 1494 1503 1512
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

 P F N F Q A A Y G L S D Q L A Q A I
 1521 1530 1539 1548 1557 1566
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG

 S D H Y P V E V M L K G G G P K K K
 1575
 CGC AAG GTT TGA 3'

 R K V *

Fig. 17(D)
(Sheet 3 of 3)

pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS (pAS106)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 355 a 475 c 452 g 314 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
541 GGCGCCCTGA CCAGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTGGGG AGACCAAGAT GTCCAATGCCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
1321 CAGTGGTCAT CCATCCGCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCTGAGTG ACCAACTGGC CCAAGCCATC AGTGAACACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGGC GACCAAAAAA GAAGCGCAAG GTTTGA

//

→ NLS

Fig. 18(A)

LOCUS FDDNASE106 1596 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<799..1596)
 /note="1 to 1596 of PAS106.dna [Split]"
 frag 721..798
 /note="1 to 78 of 102/106linker"
 BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCCTCAGTCCAGCCTCAGC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTGTC CAGCACCAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCCTGGTCA CAGAGGTCA GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCACGT GCCTATGACA GGATCGGTGTC GTCAGGGATG
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTCCCT TTAACCTCCA GGCTGCCTAT
 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
 1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

//

Fig. 18(B)

LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<808..1605) /note="1 to 1596 of PAS106.dna [Split]"
 frag 730..807 /note="1 to 78 of 102/106linker"
 BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER
 ORIGIN -
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCTTGGTT TGCTTACTGG GGCCAAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGGCC
 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTGTC CACCGTGTCC AGCACCAAGAG
 781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGGGGA GACCAAGATG
 841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATGCCCTG
 901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCGTGGGGA AGCTGCTGGA CAACCTCAAT
 961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAAGTGAGC CACTGGGACG GAACAGCTAT
 1021 AAGGAGCGCT ACCTGTTCTG GTACAGGGCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
 1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
 1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAAG GAGTTGCCA TTGTTCCCT GCATGCCGCC
 1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
 1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
 1321 AGACCCCTCCC AGTGGTCATC CATCCGCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
 1381 CCCGACAGCG CTGACACCC AGCTACACCC ACCGACTGTG CCTATGACAG GATCGTGGGT
 1441 GCAGGGATGC TGCTCCGAGG GGCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTCCAG
 1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
 1561 GTGATGCTGA AGGGGGCGG ACCCAAAAG AAGCGCAAGG TTTGA

//

Fig. 18(C)

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
-----	-----	-----	-----	-----	-----
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
-----	-----	-----	-----	-----	-----
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
-----	-----	-----	-----	-----	-----
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
-----	-----	-----	-----	-----	-----
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
-----	-----	-----	-----	-----	-----
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
-----	-----	-----	-----	-----	-----
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
-----	-----	-----	-----	-----	-----
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
-----	-----	-----	-----	-----	-----
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
-----	-----	-----	-----	-----	-----
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
-----	-----	-----	-----	-----	-----
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
-----	-----	-----	-----	-----	-----
G A L T S G V H T F P A V L Q S S G					

Fig. 18(D)

(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					

L Y S L S S V V T V P S S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					

T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					

V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG					

C P A P E G S G G L K I A A F N I Q					
819	828	837	846	855	864
ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG					

T F G E T K M S N A T L V S Y I V Q					
873	882	891	900	909	918
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG					

I L S R Y D I A L V Q E V R D S H L					
927	936	945	954	963	972
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT					

T A V G K L L D N L N Q D A P D T Y					
981	990	999	1008	1017	1026
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG					

H Y V V S E P L G R N S Y K E R Y L					
1035	1044	1053	1062	1071	1080
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT					

F V Y R P D Q V S A V D S Y Y Y D D					
1089	1098	1107	1116	1125	1134
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG					

G C E P C G N D T F N R E P A I V R					
1143	1152	1161	1170	1179	1188
TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG					

F F S R F T E V R E F A I V P L H A					
1197	1206	1215	1224	1233	1242

Fig. 18(D)
(Sheet 2 of 3)

28

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A P G D A V A E I D A L Y D V Y L D
 1251 1260 1269 1278 1287 1296
 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V Q E K W G L E D V M L M G D F N A
 1305 1314 1323 1332 1341 1350
 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G C S Y V R P S Q W S S I R L W T S
 1359 1368 1377 1386 1395 1404
 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P T F Q W L I P D S A D T T A T P T
 1413 1422 1431 1440 1449 1458
 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H C A Y D R I V V A G M L L R G A V
 1467 1476 1485 1494 1503 1512
 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V P D S A L P F N F Q A A Y G L S D
 1521 1530 1539 1548 1557 1566
 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q L A Q A I S D H Y P V E V M L K G
 1575 1584 1593
 GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3'
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G G P K K K R K V *

Fig. 18(D)

(Sheet 3 of 3)

pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(pAS107)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 448 g 314 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TCGAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGTCTG TGTGGAGTGC CCACCGTGC CAAGCACCTGA AGGCAGGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATT GGGGAGACCA AGATGTCCTAA TGCCACCCCTC
841 GTCAGCTACA TTGTGAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTAGA
901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACCGAAC GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGGC GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCC GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCAAC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCAAGC CATCAGTGCAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
1561 GGCGGACCCA AAAAGAAGCG CAAGGGTTGA

//

→ NLS

Fig. 19(A)

LOCUS FDDNASE107 1590 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1590)
 /note="1 to 1590 of PAS107.dna [Split]"
 frag 721..792
 /note="1 to 72 of 103/107linker"
 frag join(721..>771,<772..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 354 A 473 C 448 G 315 T 0 OTHER
 ORIGIN -
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGGC TACTGGATAG AGTGGGTGCG CCAGGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
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 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
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 541 GCGGCCCTGA CCAGCGGCCT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGT CAGCACCCAGA GGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGC GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCACTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTTT CCCTTTAAGT TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCAAGC CATCAGTGC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
 1561 GGCAGACCCA AAAAGAAGCG CAAGGTTTGA

//

Fig. 19(B)

LOCUS FDDNASE107 1599 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<802..1599)
 /note="1 to 1590 of PAS107.dna [Split]"
 frag 730..801
 /note="1 to 72 of 103/107linker"
 frag join(730..>780,<781..801)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCCT GCAAGGCTTC TGGCTACACC TTCACTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCTCTGGTT TGCTTACTGG GGCAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CGGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGGGTG CACACCTTCC CGGCTGTCCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGAAC GTGCCCTCCA GCAGCTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTGAGTGTC CACCGTGTCC AGCACCAGAG
 781 GGCAGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTG GGGAGACCAA GATGTCCAAT
 841 GCCACCCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
 901 GAGGTCAGAG ACAGGCCACCT GACTGCCGTG GGGAAAGCTGC TGGACAACCT CAATCAGGAC
 961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
 1021 CGCTACCTGT TCGTGTACAG GCCTGACCAAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAAGGTT
 1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTT CCCTGCATGC GGCCCCGGGG
 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
 1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
 1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
 1381 AGCGCTGACA CCACAGCTAC ACCCACGCCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
 1441 ATGCTGCTCC GAGGGGCCGT TGTGCTCCGAC TCAGTCTTCC CCTTTAACTT CCAGGCTGCC
 1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGCAC ACTATCCAGT GGAGGTGATG
 1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

//

Fig. 19(C)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC

9 18 27 36 45 54

M G W S C I I L F L V A T A T G V H

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

63 72 81 90 99 108

S Q V Q L V Q S G A E V K K P G A S

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

117 126 135 144 153 162

V K V S C K A S G Y T F S A Y W I E

TGG GTG CGC CAG GCT CCA CGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

171 180 189 198 207 216

W V R Q A P G K G L E W V G E I L P

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

225 234 243 252 261 270

G S N N S R Y N E K F K G R V T V T

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

279 288 297 306 315 324

R D T S T N T A Y M E L S S L R S E

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

333 342 351 360 369 378

D T A V Y Y C A R S Y D F A W F A Y

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

387 396 405 414 423 432

W G Q G T L V T V S S A S T K G P S

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

441 450 459 468 477 486

V F P L A P S S K S T S G G T A A L

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

495 504 513 522 531 540

G C L V K D Y F P E P V T V S W N S

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

549 558 567 576 585 594

G A L T S G V H T F P A V L Q S S G

Fig. 19(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
-----	-----	-----	-----	-----	-----
C P A P E G G L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
-----	-----	-----	-----	-----	-----
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
-----	-----	-----	-----	-----	-----
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
-----	-----	-----	-----	-----	-----
V G K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
-----	-----	-----	-----	-----	-----
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC					
-----	-----	-----	-----	-----	-----
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
-----	-----	-----	-----	-----	-----
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
-----	-----	-----	-----	-----	-----
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

Fig. 19(D)
(Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA

 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC

 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC

 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT

 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC

 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG

 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557 1566
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA

 A Q A I S D H Y P V E V M L K G G G
 1575 1584
 CCC AAA AAG AAG CGC AAG GTT TGA 3'

 P K K K R K V *

Fig. 19(D)
(Sheet 3 of 3)

Mammalian expression of humanised HMFG1-D Nase constructs

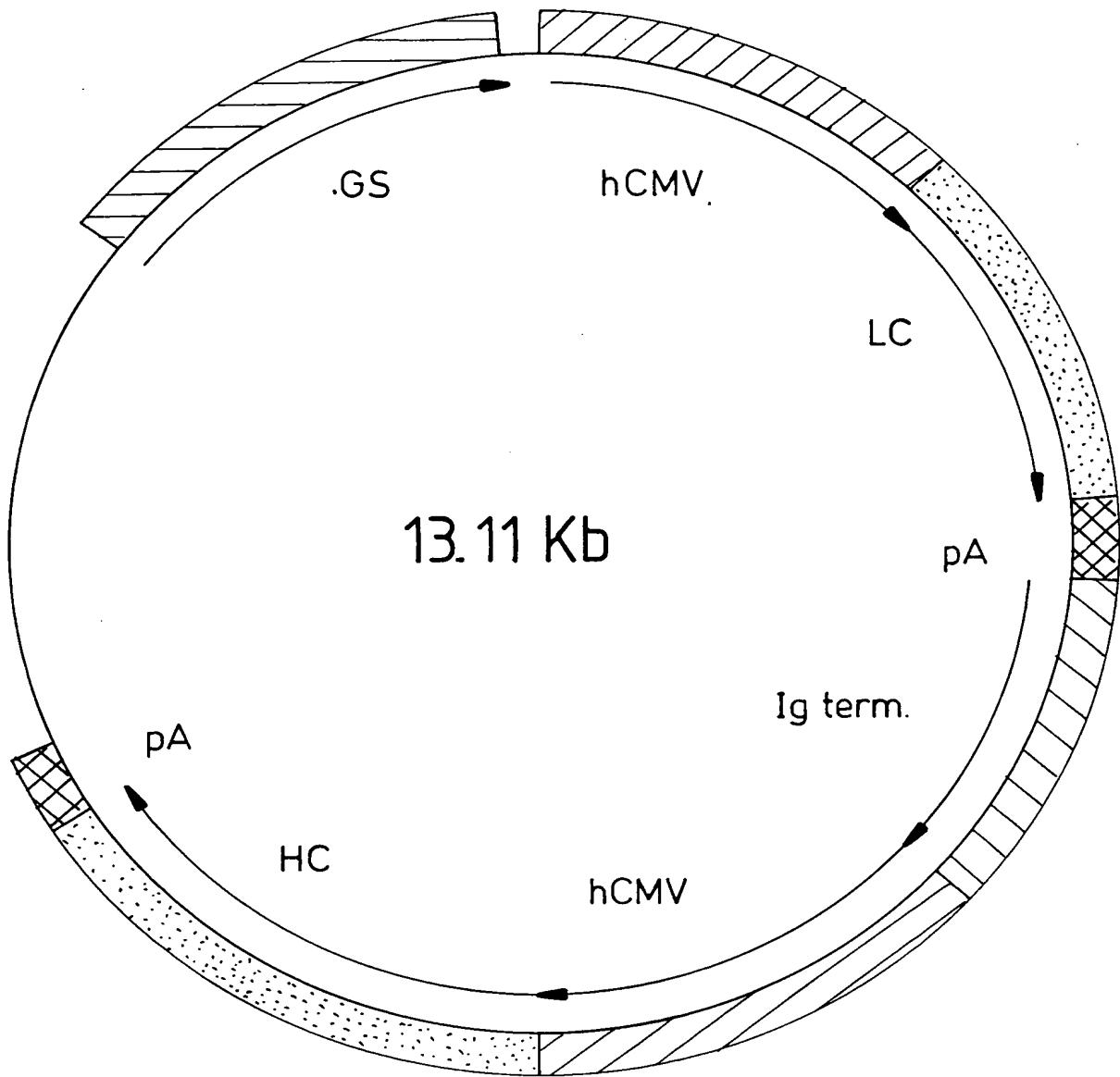


Fig. 20

Immuno-precipitation of metabolically labelled transient transfectants

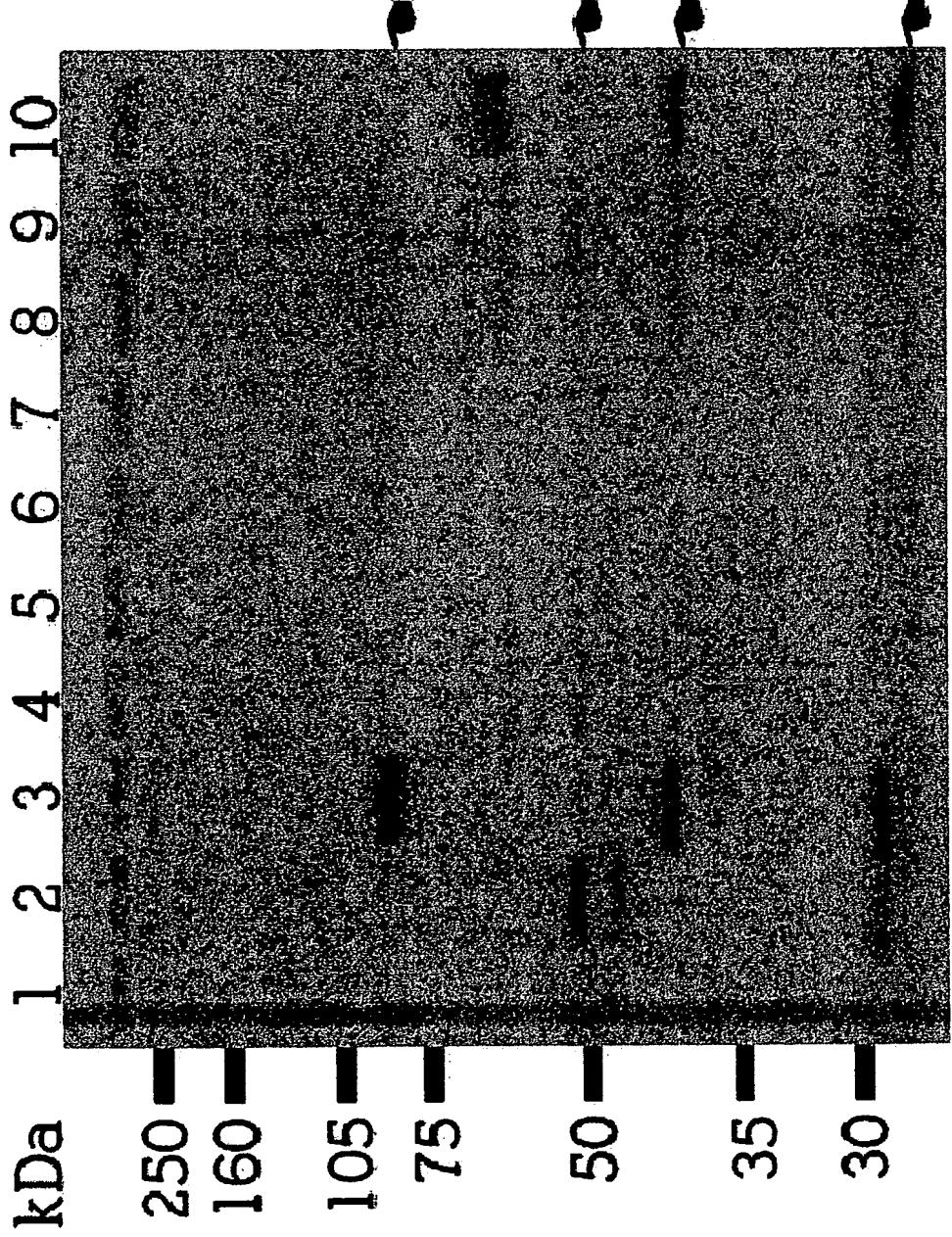


Fig. 21(A)

8% SDS-PAGE reducing gel

Immuno-precipitation of metabolically labelled transient transfectants

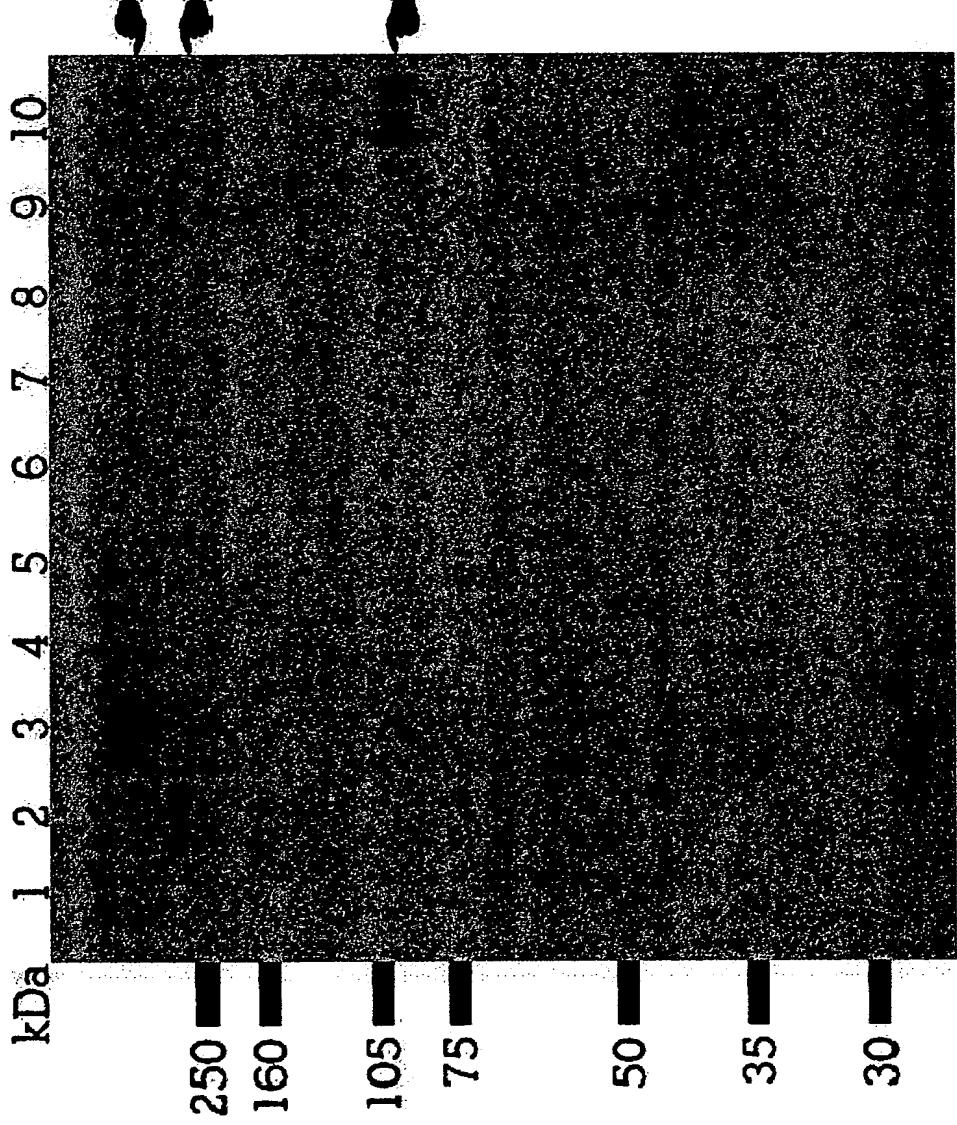


Fig. 21(B)

8% SDS-PAGE non-reducing gel

Immuno-precipitation of metabolically labelled transient transfectants

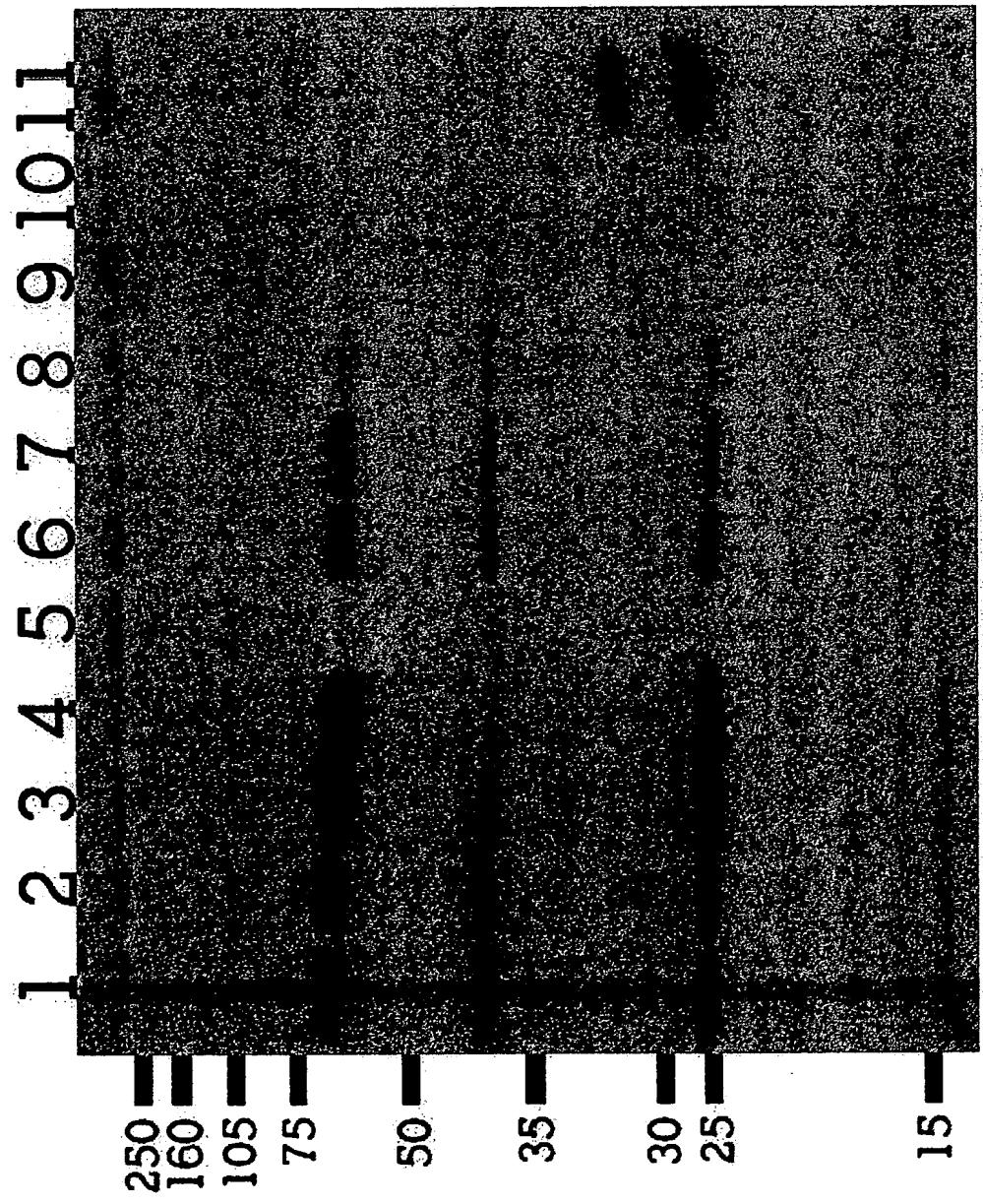


Fig. 21(C) 10% SDS-PAGE reducing gel

Fig. 21(D)

8% SDS-PAGE non-reducing gel

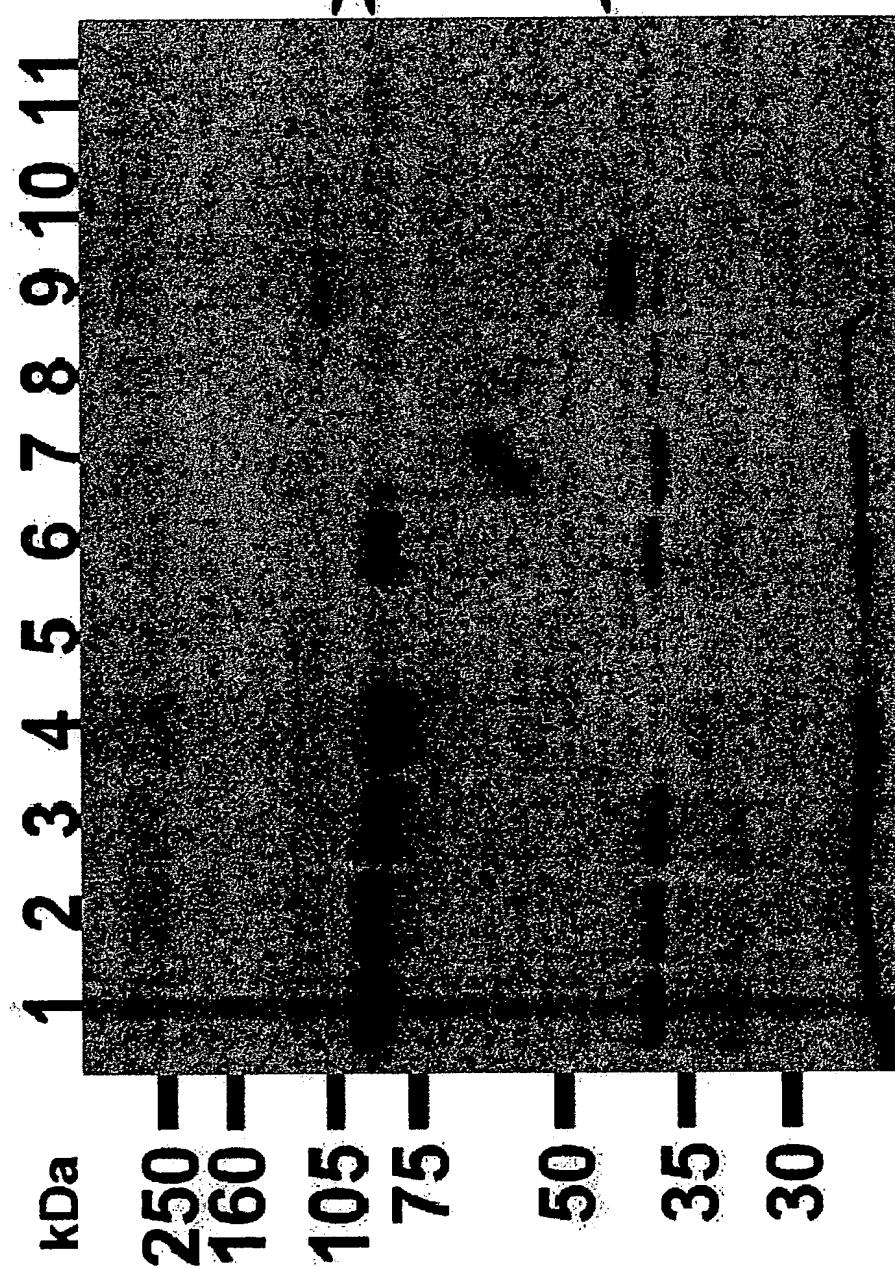


Fig. 22

PDTTRP binding assay standard curve (5' development)

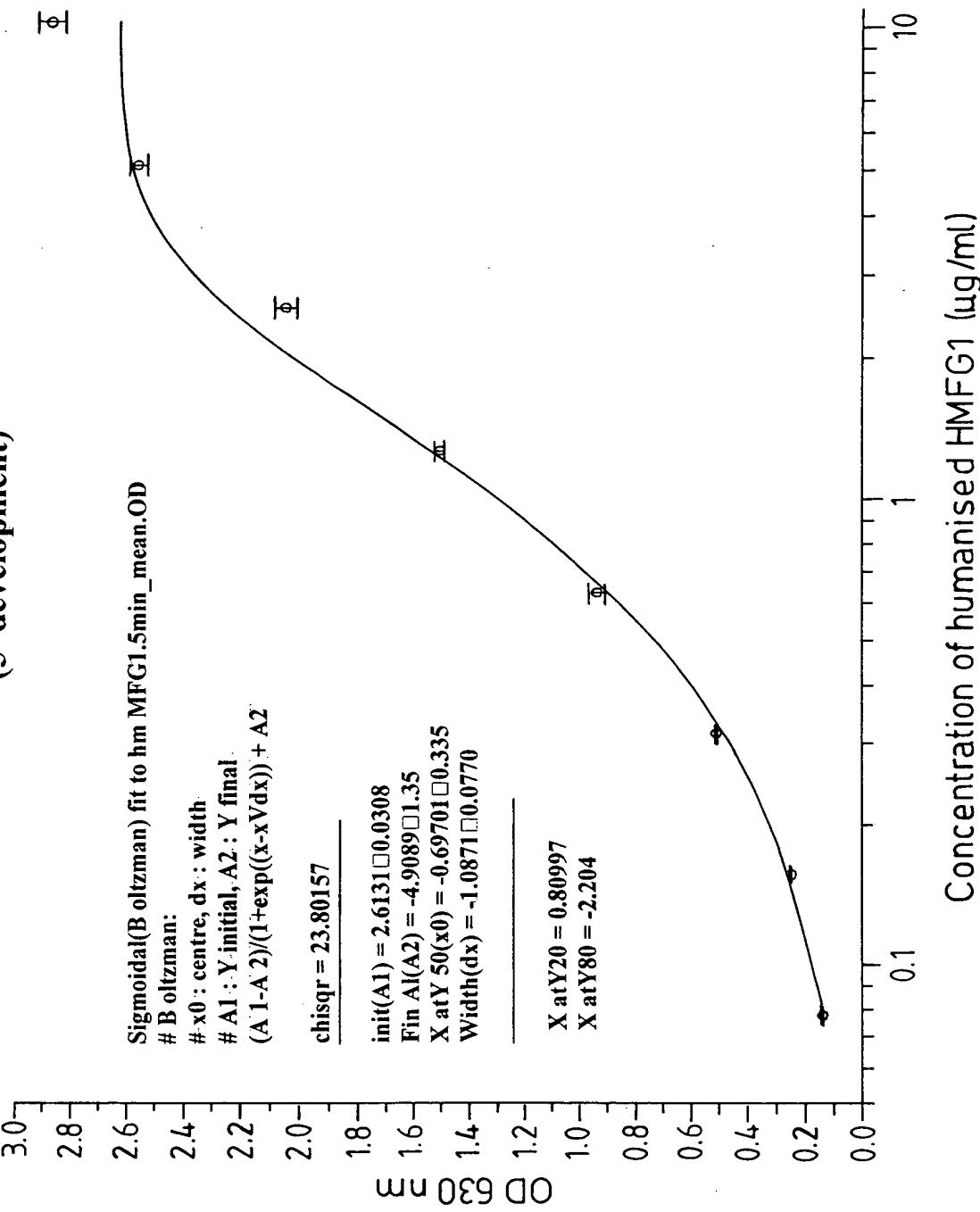
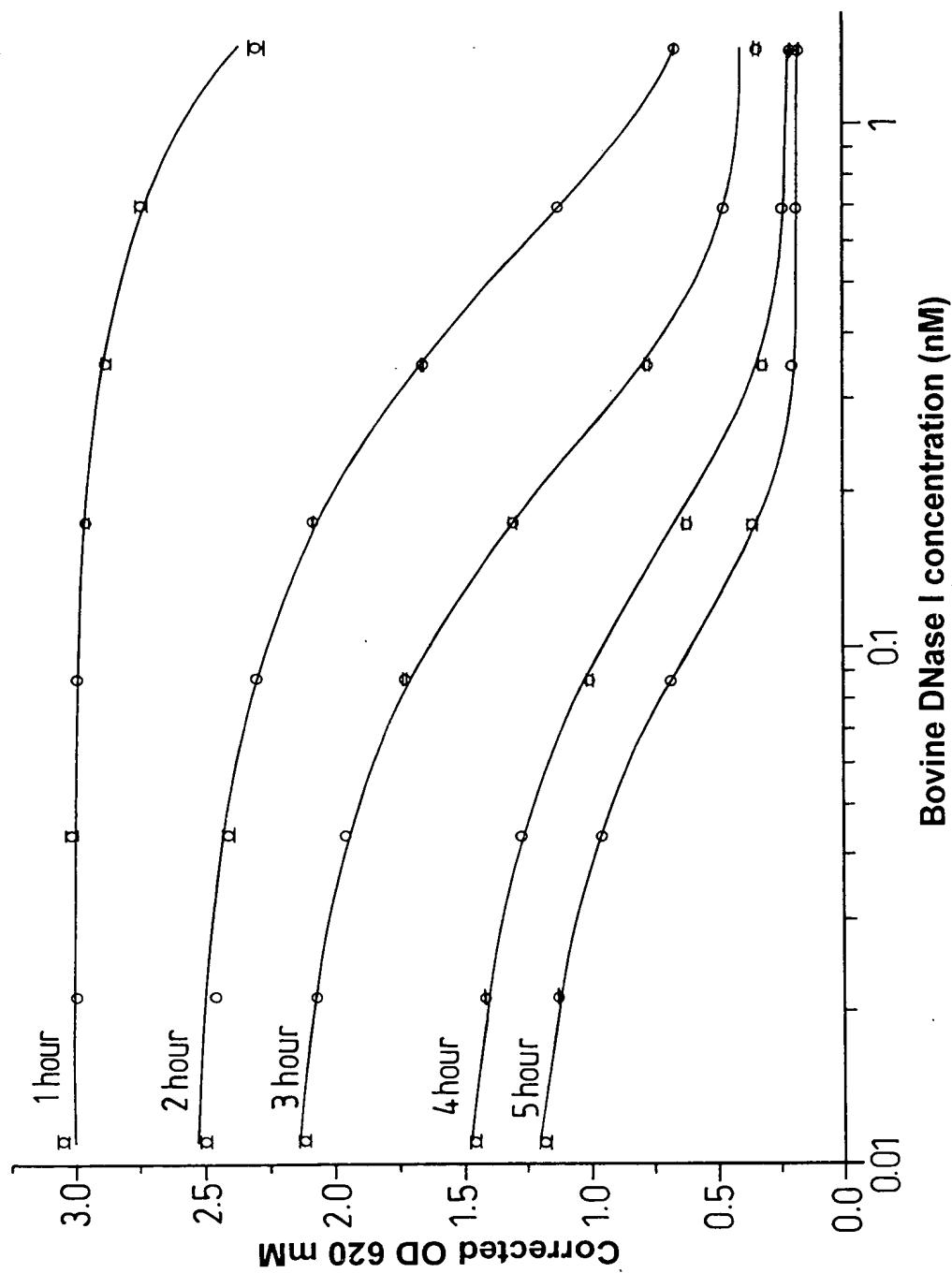


Fig. 23

Corrected bovine DNase I standard curves
at various time points



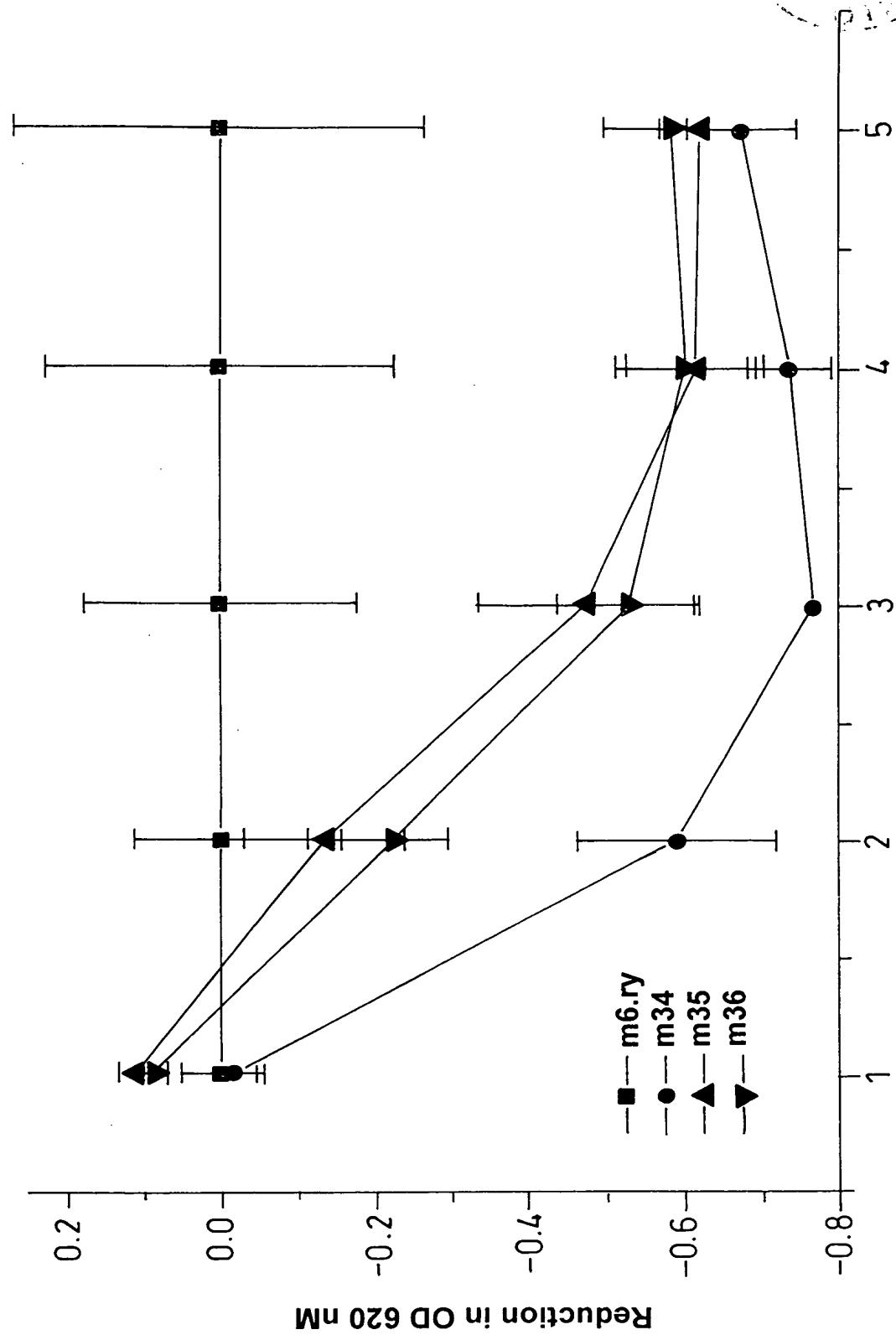


Fig. 24

Corrected DNase I activity in transiently expressed
humanised HMFG1 F(ab')2-human DNase I fusions

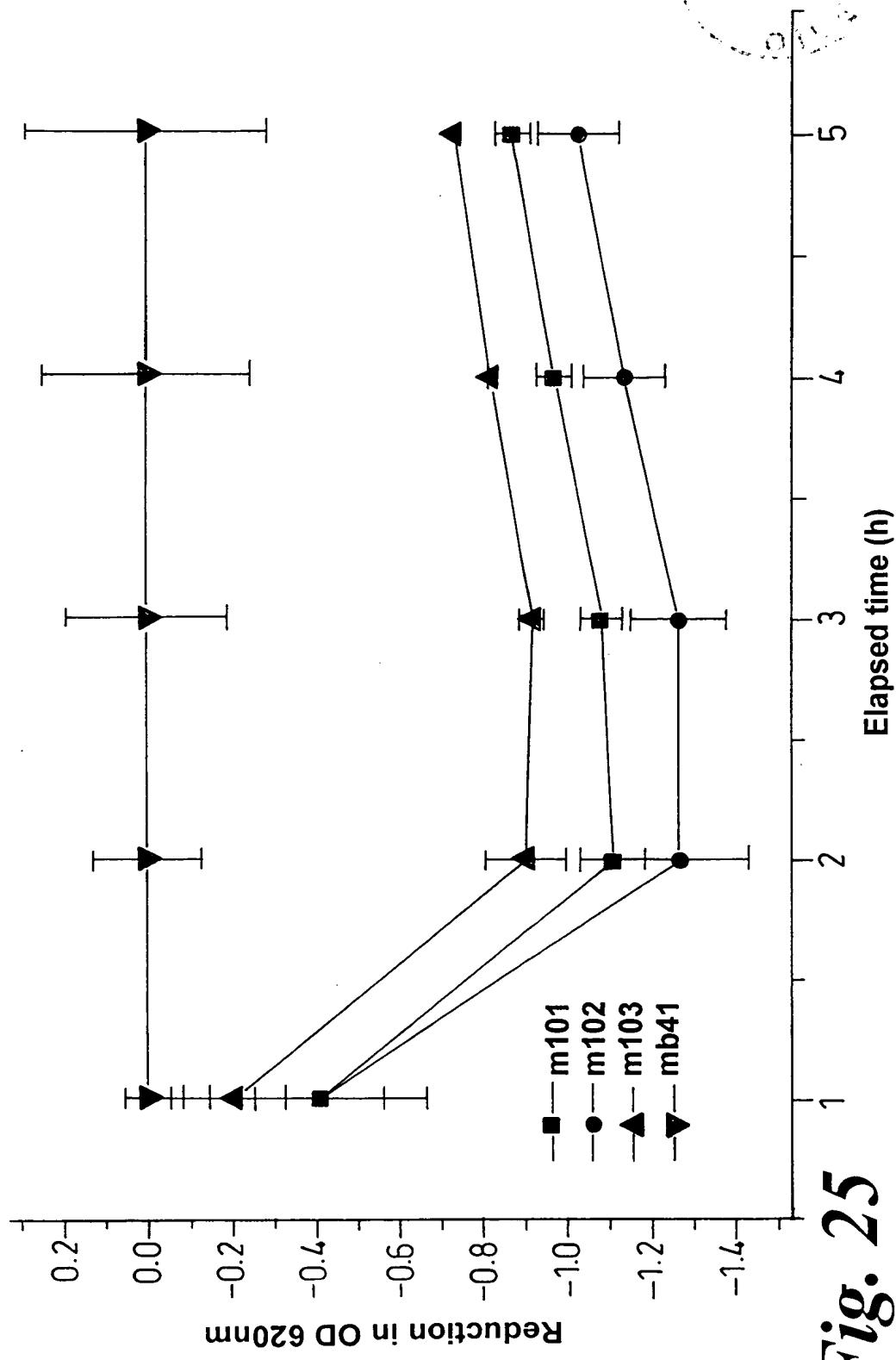
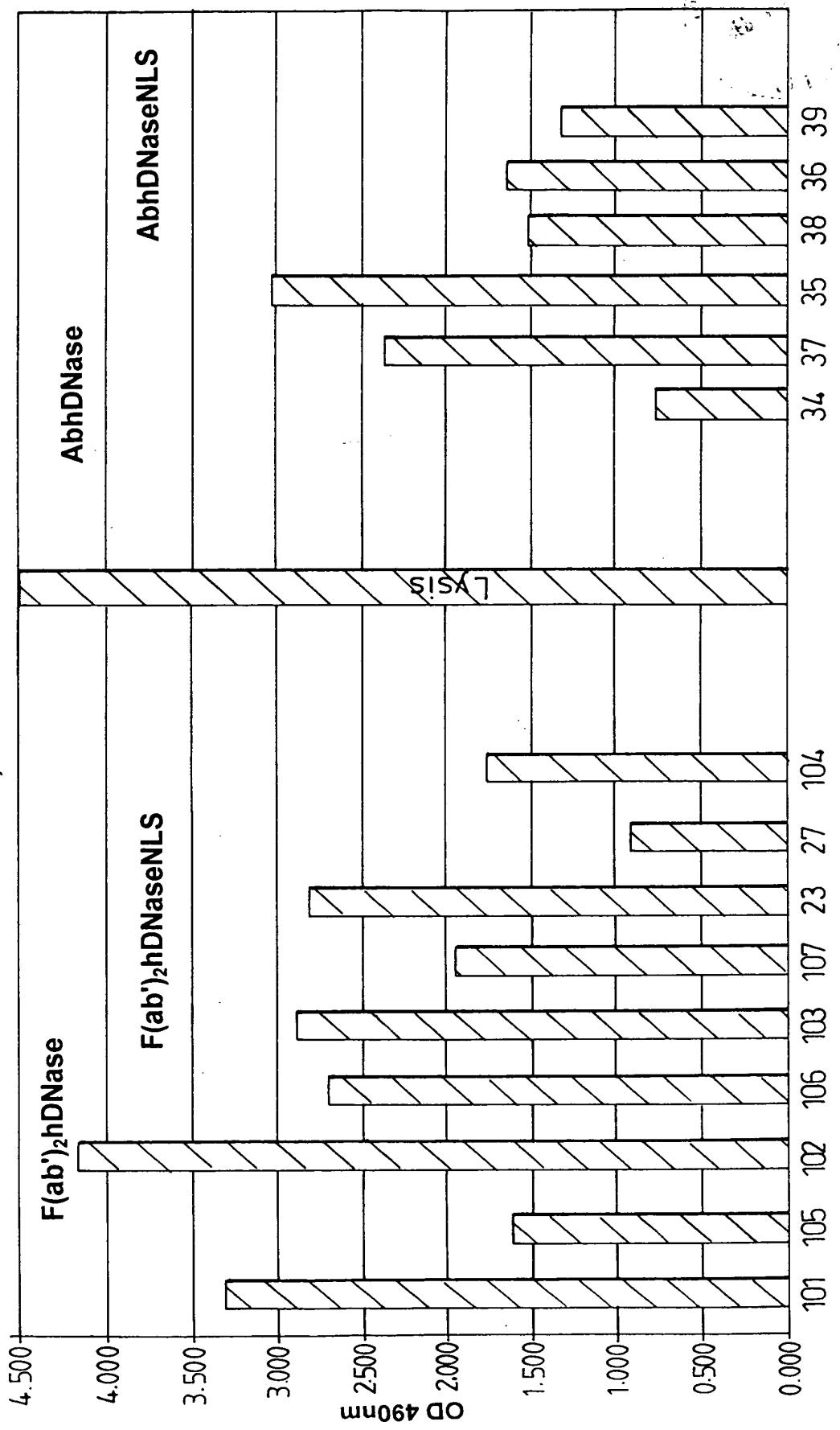


Fig. 25

Fig. 26

Cytotoxicity Assay
10,000 cells/Well



0.097 μ g/ml of each construct

Fig. 27

MCF7 cells killed after 1h incubation with 1.35 ng of sample

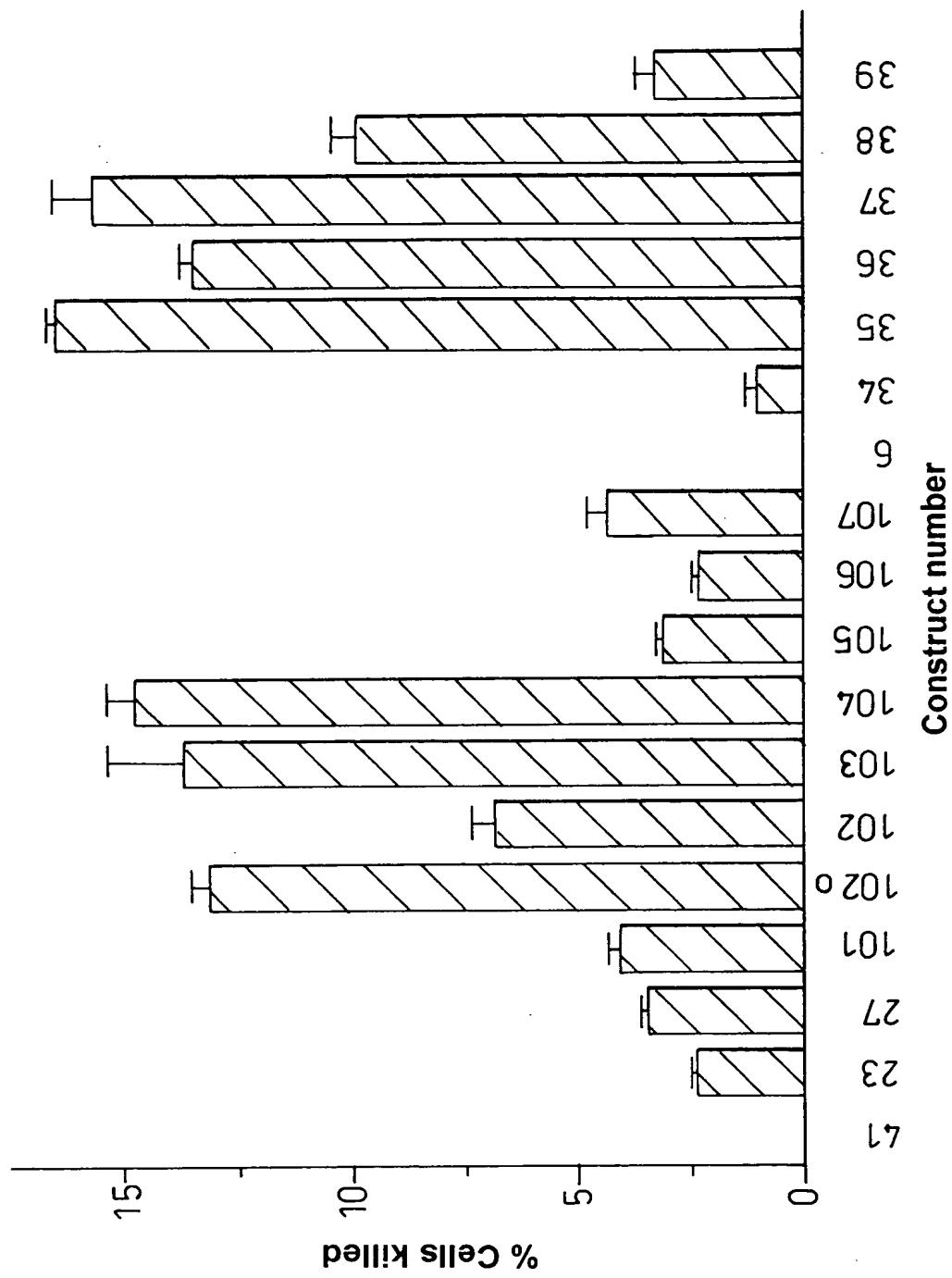
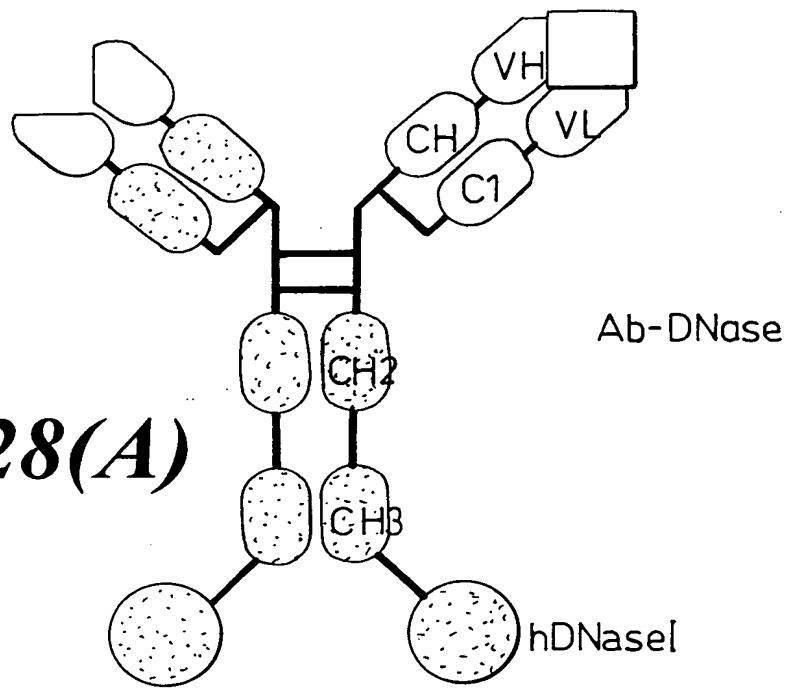


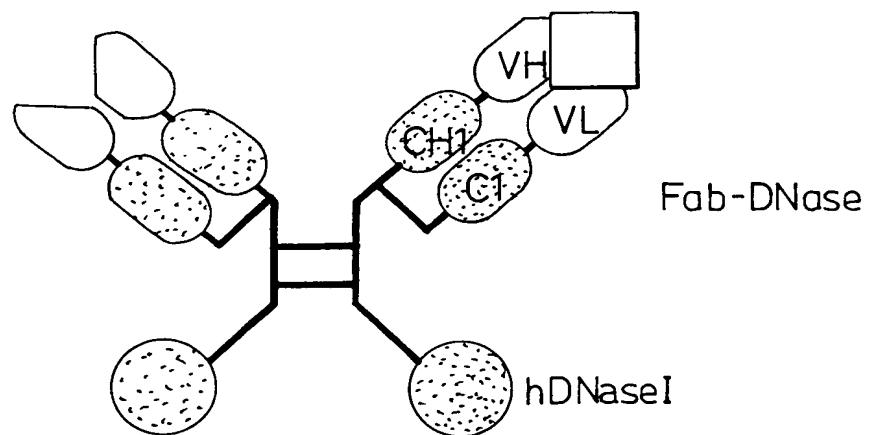
Fig. 28(A)



Ab-DNase

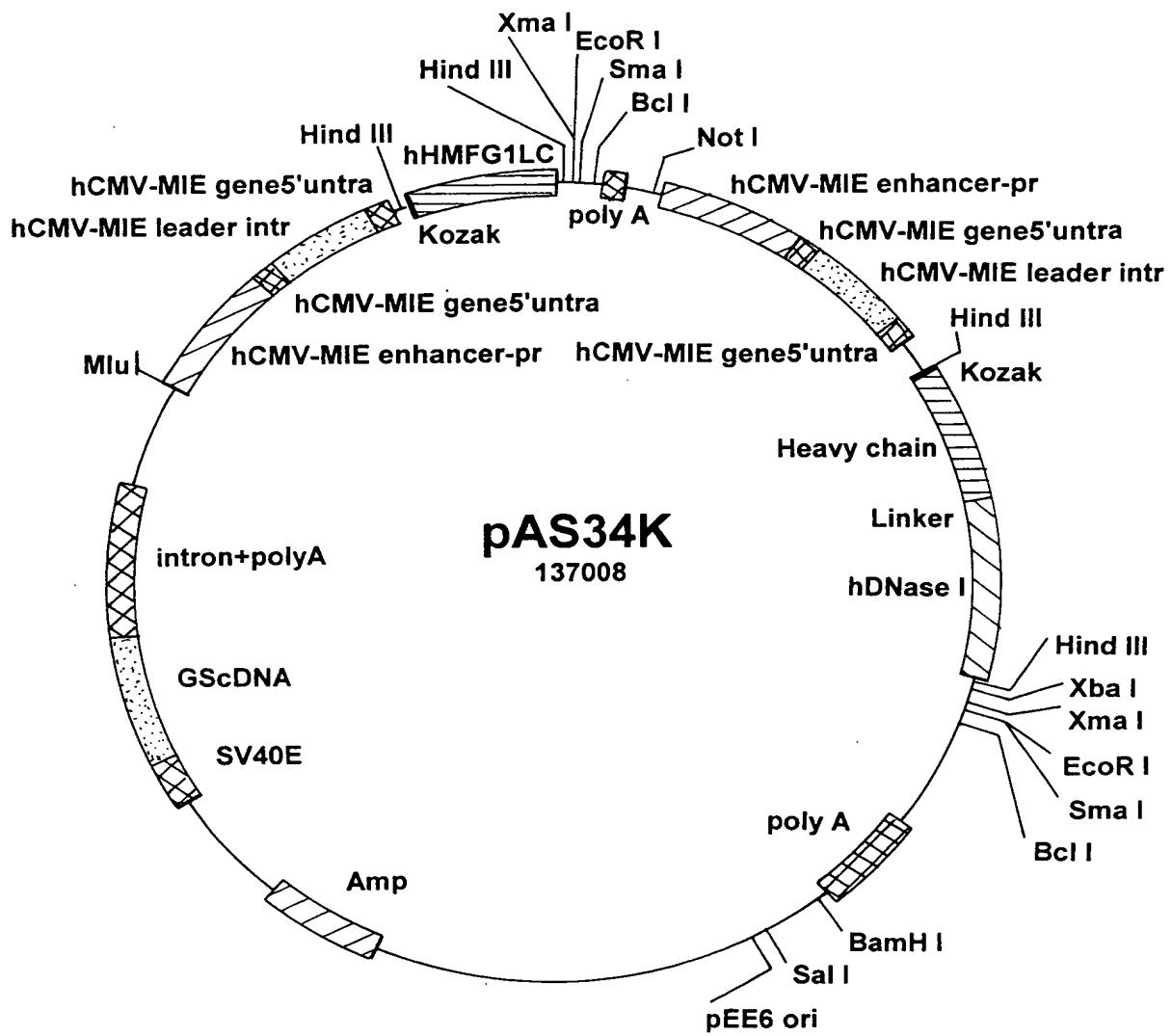
hDNaseI

Fig. 28(B)



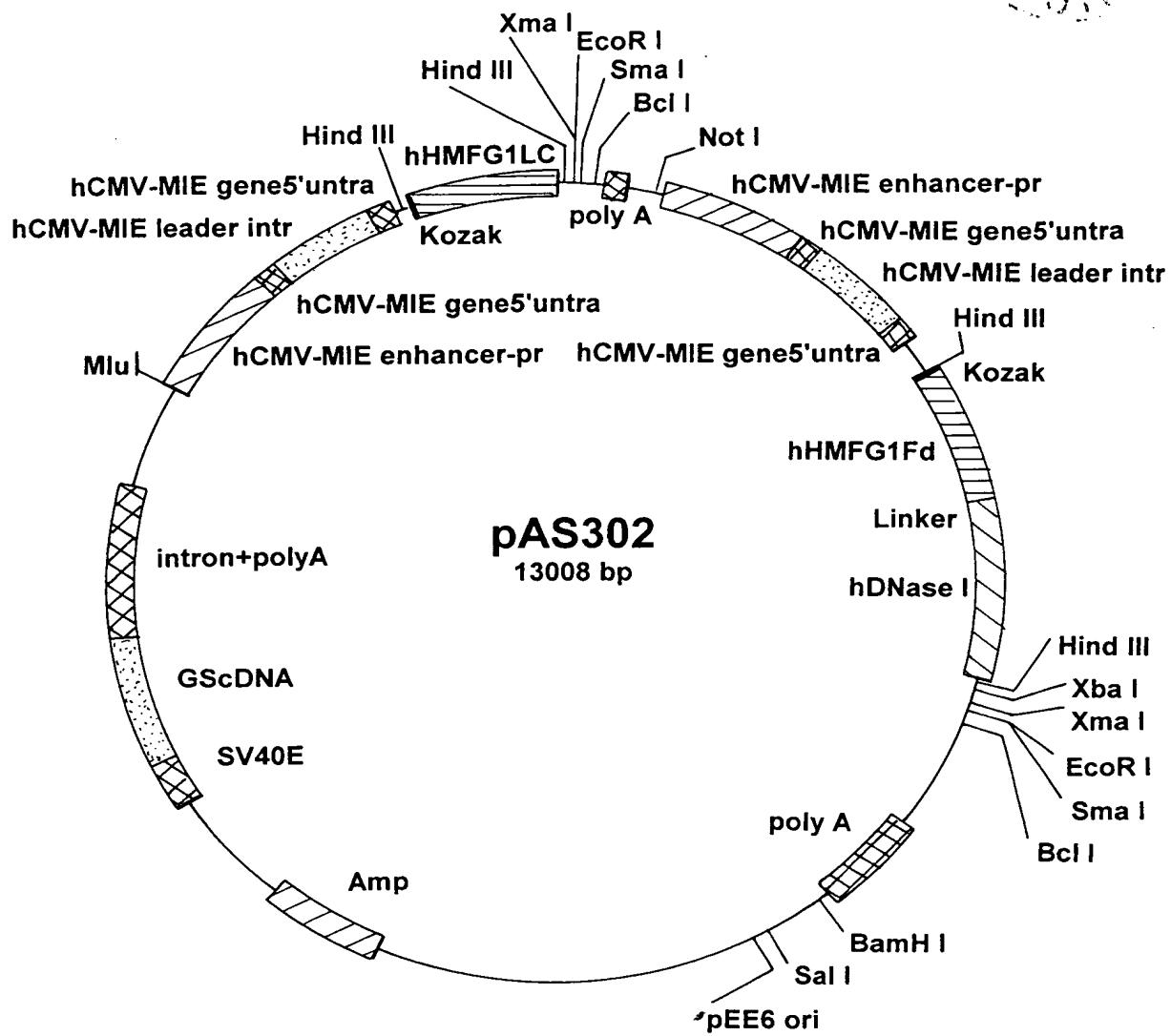
Fab-DNase

hDNaseI



Ab-DNase

Fig. 29



Fab-DNase

Fig. 30

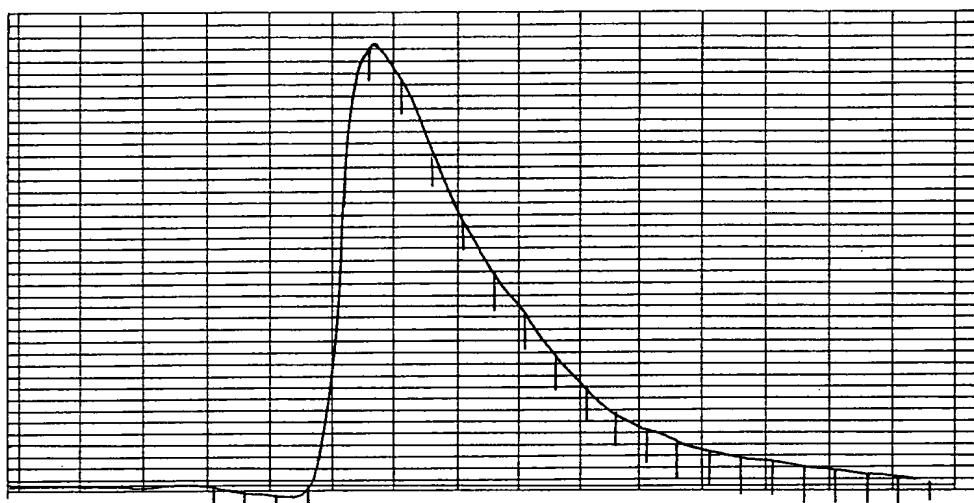


Fig. 31(A)

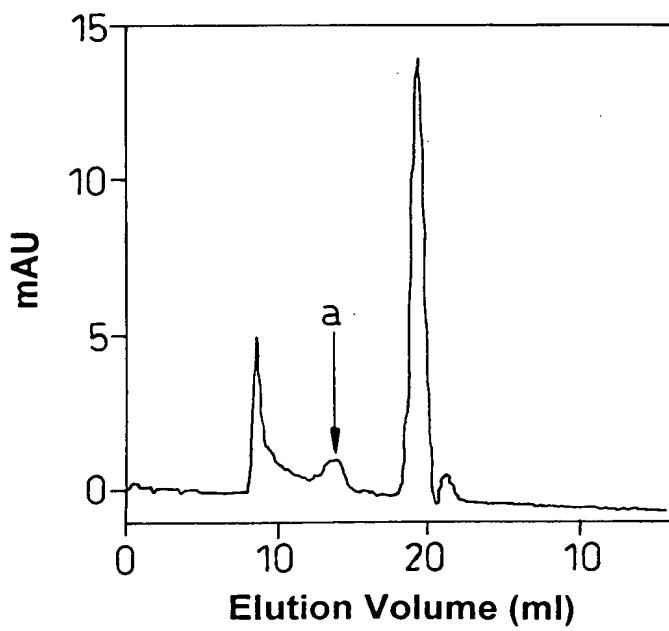


Fig. 31(B)

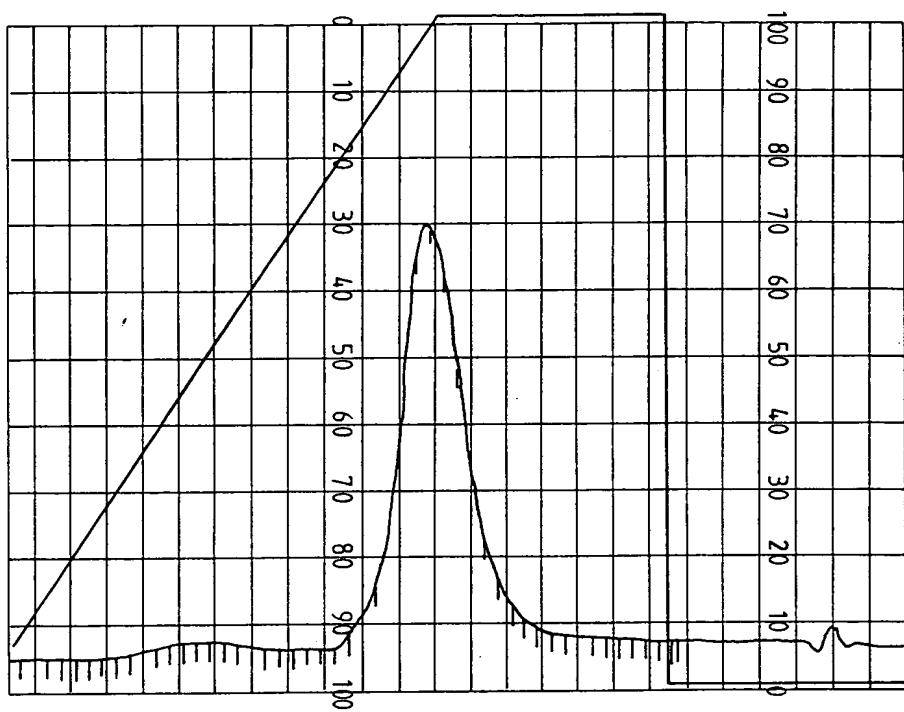


Fig. 32(A)

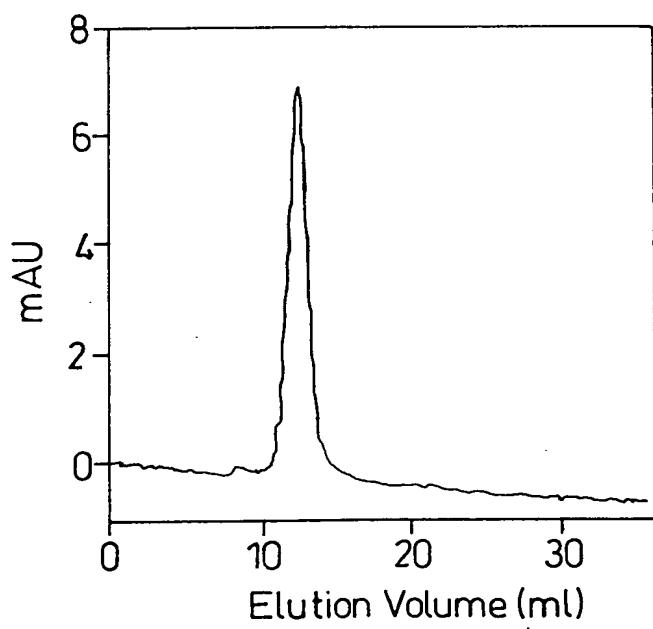


Fig. 32(B)

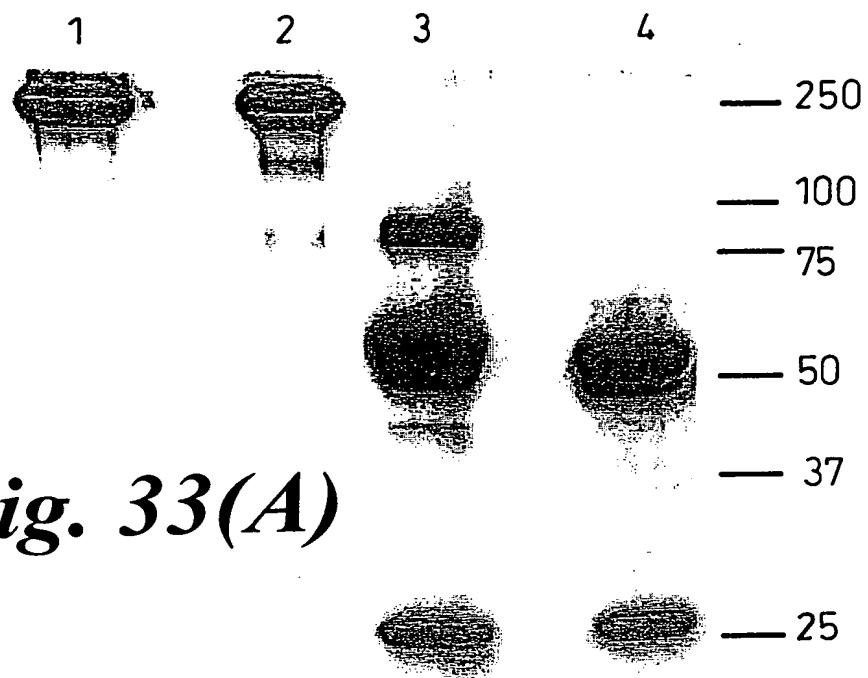


Fig. 33(A)

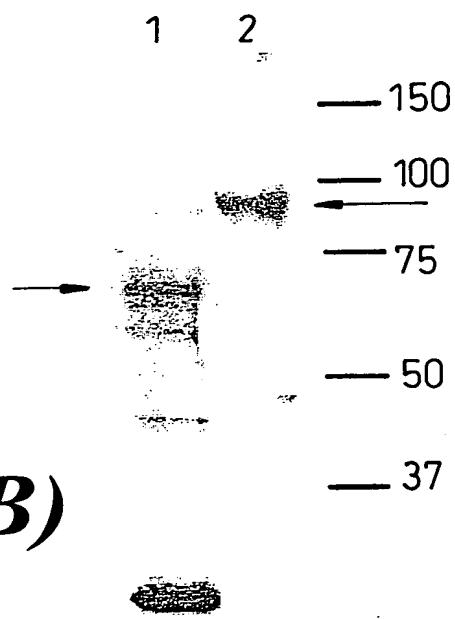


Fig. 33(B)

Bovine DNase I standard curves at various time points

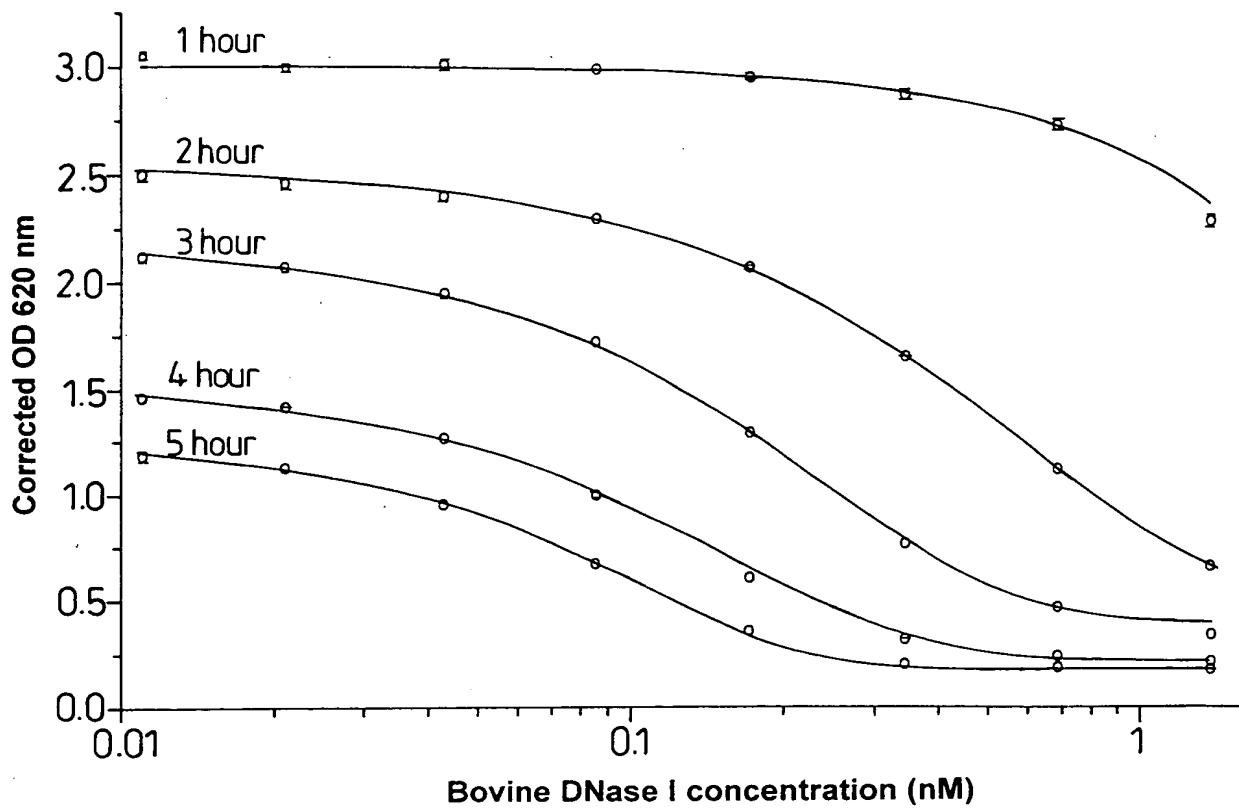


Fig. 34(A)

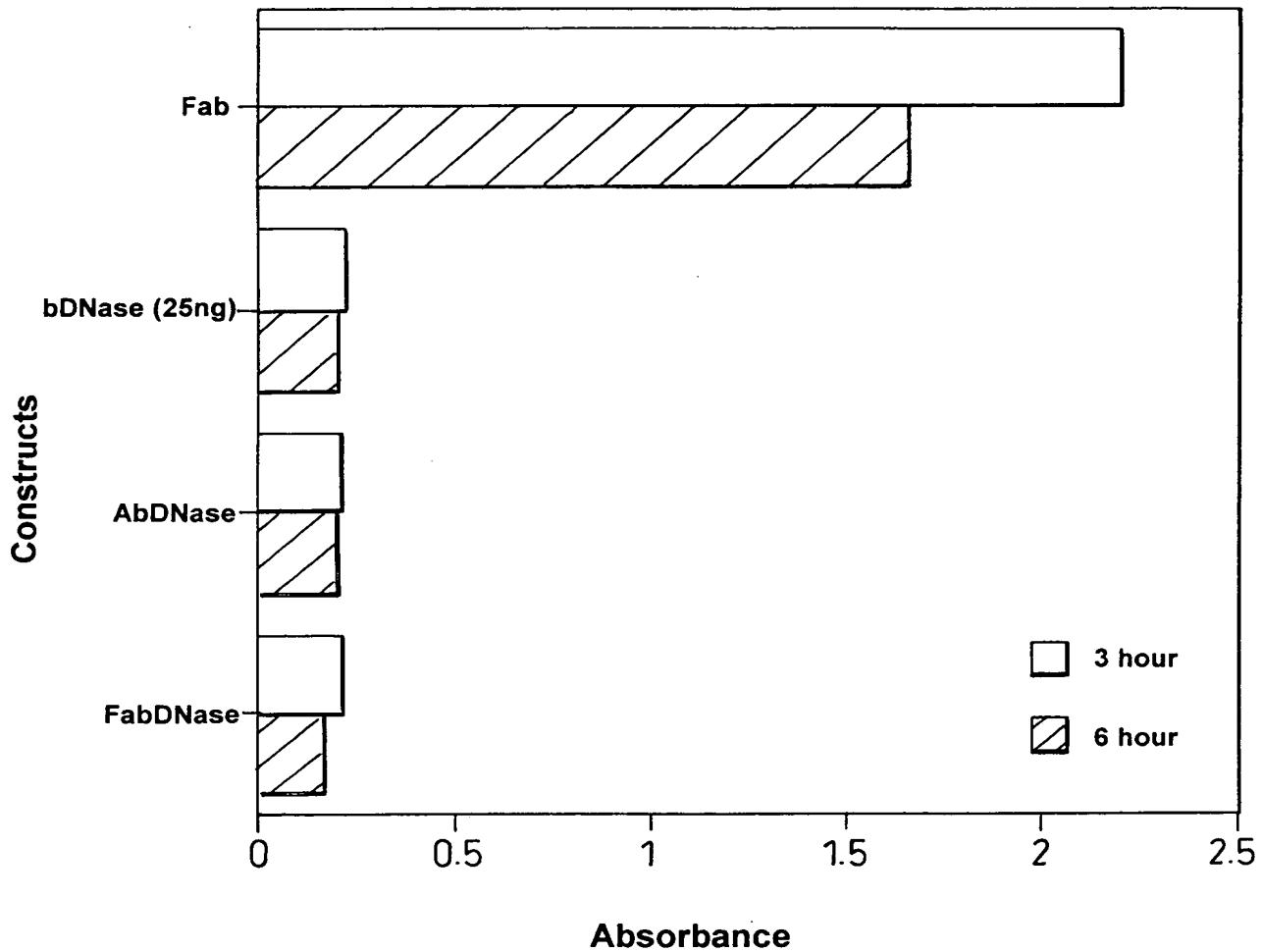


Fig. 34(B)

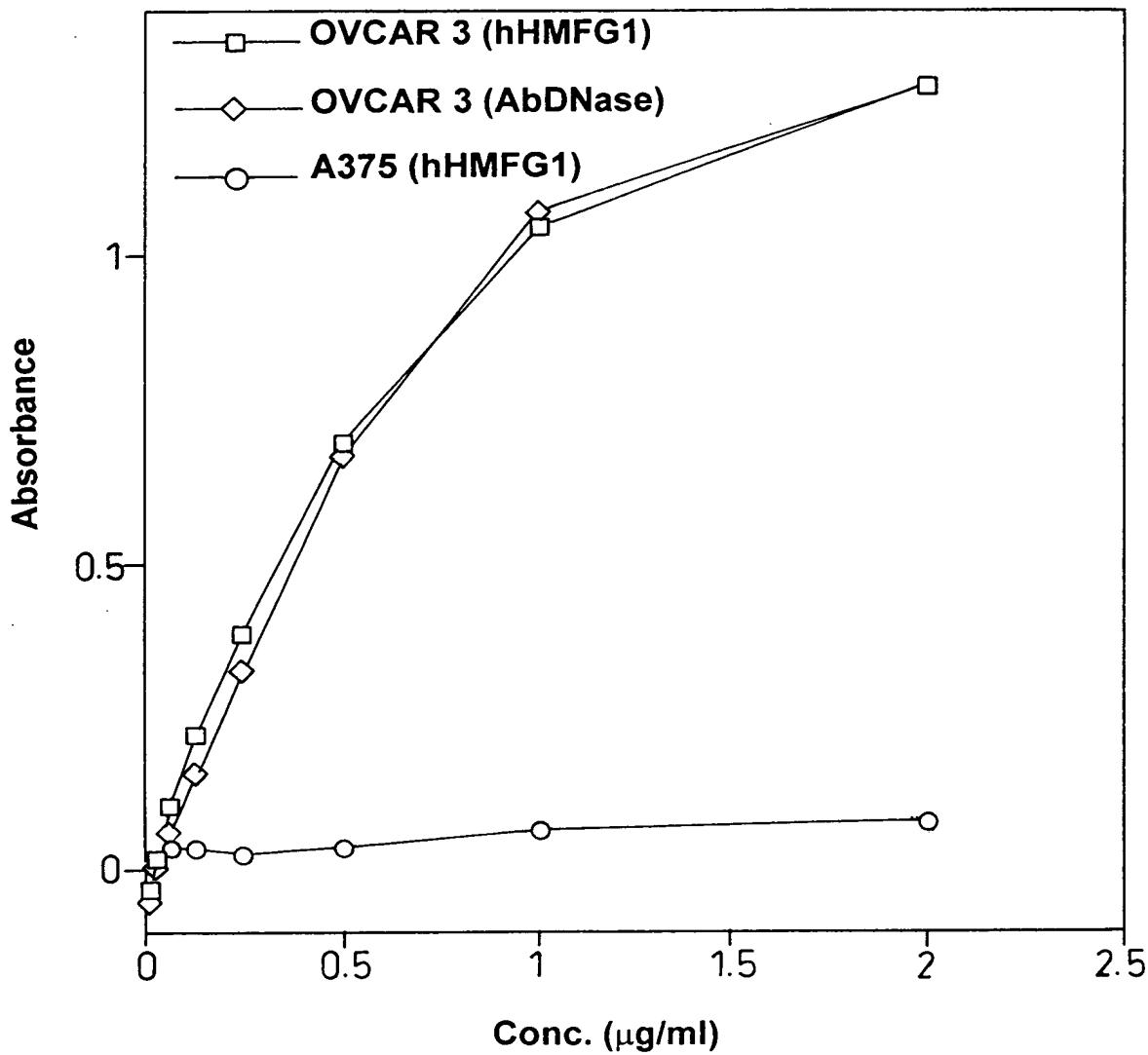


Fig. 35(A)

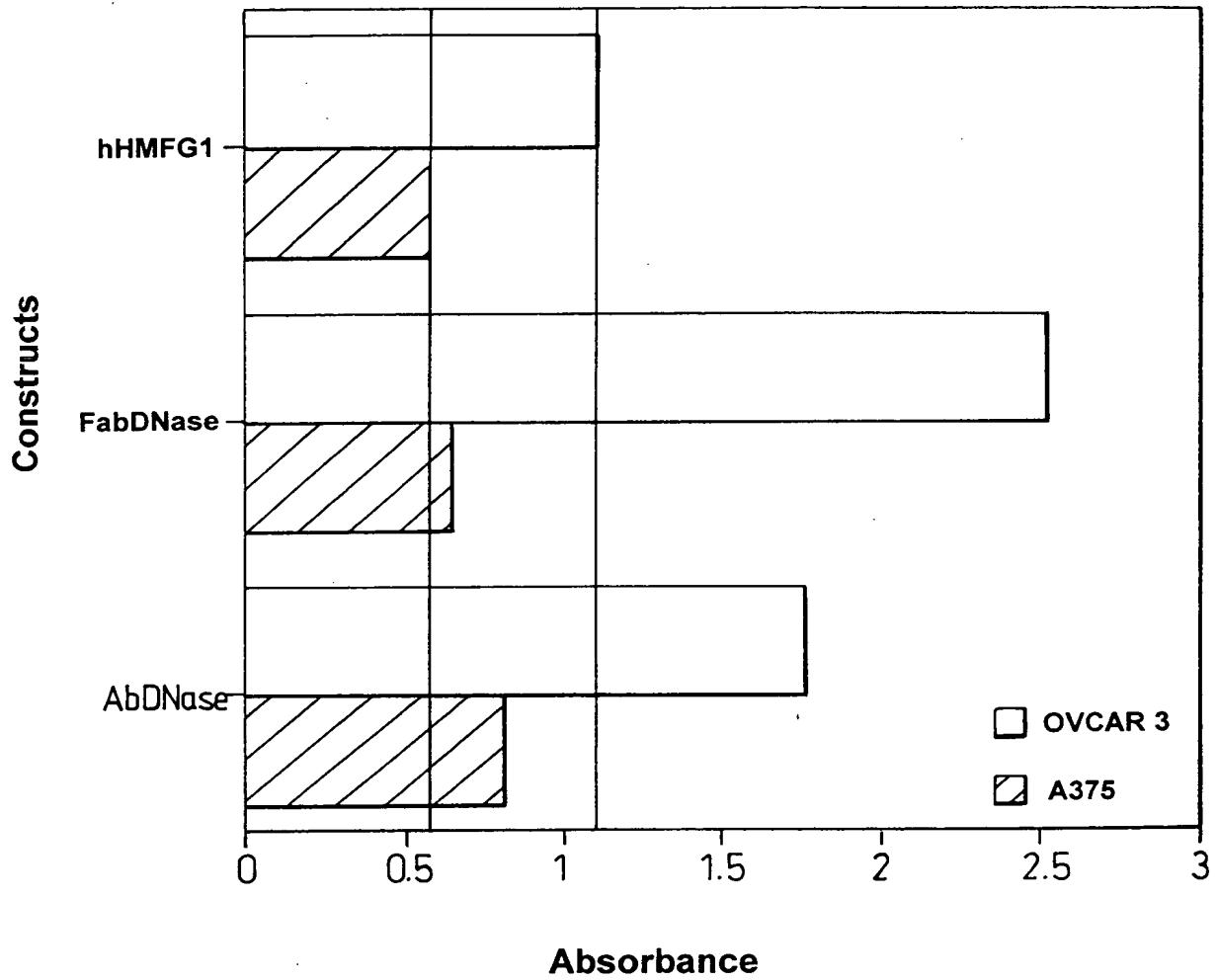


Fig. 35(B)